APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

	1				50
A. terreus 9A-1	KhsDCNSVDh	GYQCFPELSH	kWGlYAPYFS	LQDESPFPlD	VPEDChITFV
A. terreus cbs	NhsDCTSVDr	GYQCFPELSH	kWGlYAPYFS	LQDESPFPlD	VPDDChITFV
A. niger var. *awamori*	NqsTCDTVDQ	GYQCFSETSH	LWGQYAPFFS	LANESAISPD	VPAGCrVTFA
A. niger T213	NqsSCDTVDQ	GYQCFSETSH	LWGQYAPFFS	LANESVISPD	VPAGCrVTFA
A. niger NRRL3135	NqsSCDTVDQ	GYQCFSETSH	LWGQYAPFFS	LANESVISPE	VPAGCrVTFA
A. fumigatus 13073	GSkSCDTVDl	GYQCsPATSH	LWGQYSPFFS	LEDElSVSSK	LPKDCrITLV
A. fumigatus 32722	GSkSCDTVDl	GYQCsPATSH	LWGQYSPFFS	LEDElSVSSK	LPKDCrITLV
A. fumigatus 58128	GSkSCDTVDl	GYQCsPATSH	LWGQYSPFFS	LEDElSVSSK	LPKDCrITLV
A. fumigatus 26906	GSkSCDTVDl	GYQCsPATSH	LWGQYSPFFS	LEDElSVSSK	LPKDCrITLV
A. fumigatus 32239	GSkACDTVEl	GYQCsPGTSH	LWGQYSPFFS	LEDElSVSSD	LPKDCrVTFV
E. nidulans	QNHSCNTADG	GYQCFPNVSH	VWGQYSPYFS	IEQESAISeD	VPHGCeVTFV
T. thermophilus	DSHSCNTVEG	GYQCrPEISH	sWGQYSPFFS	LADQSEISPD	VPQNCkITFV
M. thermophila	ESRPCDTpDl	GFQCgTAISH	FWGQYSPYFS	VpSElDaS..	IPDDCeVTFA
Consensus	NSHSCDTVDG	GYQCFPEISH	LWGQYSPYFS	LEDESAISPD	VPDDC-VTFV
Consensus phytase	**NSHSCDTVDG**	**GYQCFPEISH**	**LWGQYSPYFS**	**LEDESAISPD**	**VPDDCRVTFV**

	51				100
A. terreus 9A-1	QVLARHGARs	PThSKtKAYA	AtIAAIQKSA	TaFpGKYAFL	QSYNYSLDSE
A. terreus cbs	QVLARHGARs	PTDSKtKAYA	AtIAAIQKNA	TaLpGKYAFL	KSYNYSMGSE
A. niger var. *awamori*	QVLSRHGARY	PTESKgKkYS	ALIEEIQQNV	TtFDGKYAFL	KTYNYSLGAD
A. niger T213	QVLSRHGARY	PTESKgKkYS	ALIEEIQQNV	TtFDGKYAFL	KTYNYSLGAD
A. niger NRRL3135	QVLSRHGARY	PTDSKgKkYS	ALIEEIQQNA	TtFDGKYAFL	KTYNYSLGAD
A. fumigatus 13073	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 32722	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 58128	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 26906	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 32239	QVLSRHGARY	PTASKsKkYK	kLVTAIQKNA	TeFKGKFAFL	ETYNYTLGAD
E. nidulans	QVLSRHGARY	PTESKsKAYS	GLIEAIQKNA	TsFwGQYAFL	ESYNYTLGAD
T. thermophilus	QLLSRHGARY	PTSSKtElYS	QLISrIQKTA	TaYKGyYAFL	KDYrYqLGAN
M. thermophila	QVLSRHGARa	PTlKRaaSYv	DLIDrIHhGA	IsYgPgYEFL	RTYDYTLGAD
Consensus	QVLSRHGARY	PTSSK-KAYS	ALIEAIQKNA	T-FKGKYAFL	KTYNYTLGAD
Consensus phytase	**QVLSRHGARY**	**PTSSKSKAYS**	**ALIEAIQKNA**	**TAFKGKYAFL**	**KTYNYTLGAD**

	101				150
A. terreus 9A-1	ELTPFGrNQL	rDlGaQFYeR	YNALTRhInP	FVRATDASRV	hESAEKFVEG
A. terreus cbs	NLTPFGrNQL	qDlGaQFYRR	YDTLTRhInP	FVRAADSSRV	hESAEKFVEG
A. niger var. *awamori*	DLTPFGEQEL	VNSGIKFYQR	YESLTRNIIP	FIRSSGSSRV	IASGEKFIEG
A. niger T213	DLTPFGEQEL	VNSGIKFYQR	YESLTRNIIP	FIRSSGSSRV	IASGEKFIEG
A. niger NRRL3135	DLTPFGEQEL	VNSGIKFYQR	YESLTRNIVP	FIRSSGSSRV	IASGKKFIEG
A. fumigatus 13073	DLTPFGEQQL	VNSGIKFYQR	YKALARSVVP	FIRASGSDRV	IASGEKFIEG
A. fumigatus 32722	DLTPFGEQQL	VNSGIKFYQR	YKALARSVVP	FIRASGSDRV	IASGEKFIEG
A. fumigatus 58128	DLTPFGEQQL	VNSGIKFYQR	YKALARSVVP	FIRASGSDRV	IASGEKFIEG
A. fumigatus 26906	DLTAFGEQQL	VNSGIKFYQR	YKALARSVVP	FIRASGSDRV	IASGEKFIEG
A. fumigatus 32239	DLTPFGEQQM	VNSGIKFYQK	YKALAgSVVP	FIRSSGSDRV	IASGEKFIEG
E. nidulans	DLTiFGENQM	VDSGaKFYRR	YKNLARKnTP	FIRASGSDRV	VASAEKFING
T. thermophilus	DLTPFGENQM	IQlGIKFYnH	YKSLARNaVP	FVRCSGSDRV	IASGrlFIEG
M. thermophila	ELTRtGQQQM	VNSGIKFYRR	YRALARKsIP	FVRTAGqDRV	VhSAENFTQG
Consensus	DLTPFGENQM	VNSGIKFYRR	YKALARK-VP	FVRASGSDRV	IASAEKFIEG
Consensus phytase	**DLTPFGENQM**	**VNSGIKFYRR**	**YKALARKIVP**	**FIRASGSDRV**	**IASAEKFIEG**

Fig. 1a

	151				200
A. terreus 9A-1	FQTARqDDHh	ANpHQPSPrV	DVaIPEGSAY	NNTLEHSlCT	AFES...STV
A. terreus cbs	FQNARqGDPh	ANpHQPSPrV	DVVIPEGTAY	NNTLEHSICT	AFEA...STV
A. niger var. *awamori*	FQSTKLkDPr	AqpgQSSPkI	DVVISEASSs	NNTLDPGTCT	VFED...SEL
A. niger T213	FQSTKLkDPr	AqpgQSSPkI	DVVISEASSs	NNTLDPGTCT	VFED...SEL
A. niger NRRL3135	FQSTKLkDPr	AqpgQSSPkI	DVVISEASSs	NNTLDPGTCT	VFED...SEL
A. fumigatus 13073	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF	NNTLDHGVCT	kFEA...SQL
A. fumigatus 32722	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF	NNTLDHGVCT	kFEA...SQL
A. fumigatus 58128	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF	NNTLDHGVCT	kFEA...SQL
A. fumigatus 26906	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF	NNTLDHGVCT	kFEA...SQL
A. fumigatus 32239	FQqANVADPG	A.TNRAAPVI	SVIIPESETY	NNTLDHSVCT	NFEA...SEL
E. nidulans	FRKAQLhDHG	S..gQATPVV	NVIIPEiDGF	NNTLDHSTCV	SFEN...DEr
T. thermophilus	FQSAKVlDPh	SDkHDAPPTI	NVIIeEGPSY	NNTLDtGSCP	VFED...SSg
M. thermophila	FHSAlLADRG	STvRPTlPyd	mVVIPETAGa	NNTLHNDlCT	AFEEgpySTI
Consensus	FQSAKLADPG	S-PHQASPVI	NVIIPEGSGY	NNTLDHGTCT	AFED---SEL
Consensus phytase	**FQSAKLADPG**	**SQPHQASPVI**	**DVIIPEGSGY**	**NNTLDHGTCT**	**AFED...SEL**

	201				250
A. terreus 9A-1	GDDAvANFTA	VFAPAIaQRL	EADLPGVqLS	TDDVVnLMAM	CPFETVSlTD
A. terreus cbs	GDAAADNFTA	VFAPAIakRL	EADLPGVqLS	ADDVVnLMAM	CPFETVSlTD
A. niger var. *awamori*	ADTVEANFTA	TFAPSIRQRL	ENDLSGVTLT	DTEVTyLMDM	CSFDTIStST
A. niger T213	ADTVEANFTA	TFAPSIRQRL	ENDLSGVTLT	DTEVTyLMDM	CSFDTIStST
A. niger NRRL3135	ADTVEANFTA	TFVPSIRQRL	ENDLSGVTLT	DTEVTyLMDM	CSFDTIStST
A. fumigatus 13073	GDEVAANFTA	lFAPDIRARa	EkHLPGVTLT	DEDVVsLMDM	CSFDTVARTS
A. fumigatus 32722	GDEVAANFTA	lFAPDIRARa	EkHLPGVTLT	DEDVVsLMDM	CSFDTVARTS
A. fumigatus 58128	GDEVAANFTA	lFAPDIRARa	EkHLPGVTLT	DEDVVsLMDM	CSFDTVARTS
A. fumigatus 26906	GDEVAANFTA	lFAPDIRARa	KkHLPGVTLT	DEDVVsLMDM	CSFDTVARTS
A. fumigatus 32239	GDEVEANFTA	lFAPAIRARI	EkHLPGVqLT	DDDVVsLMDM	CSFDTVARTA
E. nidulans	ADEiEANFTA	IMGPPIRkRL	ENDLPGIKLT	NENVIyLMDM	CSFDTMARTA
T. thermophilus	GHDAQEKFAk	qFAPAIlEKI	KDHLPGVDLA	vSDVpyLMDL	CPFETLARNh
M. thermophila	GDDAQDTYlS	TFAGPItARV	NANLPGANLT	DADTVaLMDL	CPFETVAsSS
Consensus	GDDAEANFTA	TFAPAIRARL	EADLPGVTLT	DEDVV-LMDM	CPFETVARTS
Consensus phytase	**GDDVEANFTA**	**LFAPAIRARL**	**EADLPGVTLT**	**DEDVVYLMDM**	**CPFETVARTS**

	251				300
A. terreus 9A-1	....	.DAhTLSPFC	DLFTAtEWtq	YNYLlSLDKY	YGYGGGNPLG
A. terreus cbs	....	.DAhTLSPFC	DLFTAaEWtq	YNYLlSLDKY	YGYGGGNPLG
A. niger var. *awamori*	....	.vDTKLSPFC	DLFTHdEWih	YDYLQSLkKY	YGHGAGNPLG
A. niger T213	....	.vDTKLSPFC	DLFTHdEWih	YDYLRSLkKY	YGHGAGNPLG
A. niger NRRL3135	....	.vDTKLSPFC	DLFTHdEWin	YDYLQSLkKY	YGHGAGNPLG
A. fumigatus 13073	....	.DASQLSPFC	QLFTHnEWkk	YNYLQSLGKY	YGYGAGNPLG
A. fumigatus 32722	....	.DASQLSPFC	QLFTHnEWkk	YNYLQSLGKY	YGYGAGNPLG
A. fumigatus 58128	....	.DASQLSPFC	QLFTHnEWkk	YNYLQSLGKY	YGYGAGNPLG
A. fumigatus 26906	....	.DASQLSPFC	QLFTHnEWkk	YNYLQSLGKY	YGYGAGNPLG
A. fumigatus 32239	....	.DASELSPFC	AIFTHnEWkk	YDYLQSLGKY	YGYGAGNPLG
E. nidulans	....	.HGTELSPFC	AIFTEkEWlq	YDYLQSLSKY	YGYGAGSPLG
T. thermophilus	....	.TDT.LSPFC	ALsTQeEWqa	YDYYQSLGKY	YGnGGGNPLG
M. thermophila	sdpatadagg	gNGrpLSPFC	rLFSEsEWra	YDYLQSVGKW	YGYGPGNPLG
Consensus	----------	-DATELSPFC	ALFTE-EW--	YDYLQSLGKY	YGYGAGNPLG
Consensus phytase	**..........**	**.DATELSPFC**	**ALFTHDEWRQ**	**YDYLQSLGKY**	**YGYGAGNPLG**

Fig. 1b

	301				350
A. terreus 9A-1	PVQGVGWaNE	LMARLTRAPV	HDHTCVNNTL	DASPATFPLN	ATLYADFSHD
A. terreus cbs	PVQGVGWaNE	LIARLTRSPV	HDHTCVNNTL	DANPATFPLN	ATLYADFSHD
A. niger var. *awamori*	PTQGVGYaNE	LIARLTHSPV	HDDTSSNHTL	DSNPATFPLN	STLYADFSHD
A. niger T213	PTQGVGYaNE	LIARLTHSPV	HDDTSSNHTL	DSNPATFPLN	STLYADFSHD
A. niger NRRL3135	PTQGVGYaNE	LIARLTHSPV	HDDTSSNHTL	DSSPATFPLN	STLYADFSHD
A. fumigatus 13073	PAQGIGFtNE	LIARLTRSPV	QDHTSTNsTL	vSNPATFPLN	ATMYVDFSHD
A. fumigatus 32722	PAQGIGFtNE	LIARLTRSPV	QDHTSTNsTL	vSNPATFPLN	ATMYVDFSHD
A. fumigatus 58128	PAQGIGFtNE	LIARLTRSPV	QDHTSTNsTL	vSNPATFPLN	ATMYVDFSHD
A. fumigatus 26906	PAQGIGFtNE	LIARLTRSPV	QDHTSTNsTL	vSNPATFPLN	ATMYVDFSHD
A. fumigatus 32239	PAQGIGFtNE	LIARLTNSPV	QDHTSTNsTL	DSDPATFPLN	ATIYVDFSHD
E. nidulans	PAQGIGFtNE	LIARLTQSPV	QDNTSTNHTL	DSNPATFPLD	rKLYADFSHD
T. thermophilus	PAQGVGFvNE	LIARMTHSPV	QDYTTVNHTL	DSNPATFPLN	ATLYADFSHD
M. thermophila	PTQGVGFvNE	LLARLAgvPV	RDgTSTNRTL	DGDPrTFPLG	rPLYADFSHD
Consensus	PAQGVGF-NE	LIARLTHSPV	QDHTSTNHTL	DSNPATFPLN	ATLYADFSHD
Consensus phytase	**PAQGVGFANE**	**LIARLTRSPV**	**QDHTSTNHTL**	**DSNPATFPLN**	**ATLYADFSHD**

	351				400
A. terreus 9A-1	SNLVSIFWAL	GLYNGTAPLS	qTSVESVSQT	DGYAAAWTVP	FAARAYVEMM
A. terreus cbs	SNLVSIFWAL	GLYNGTkPLS	qTTVEDITrT	DGYAAAWTVP	FAARAYIEMM
A. niger var. *awamori*	NGIISILFAL	GLYNGTkPLS	TTTVENITQT	DGFSSAWTVP	FASRlYVEMM
A. niger T213	NGIISILFAL	GLYNGTkPLS	TTTVENITQT	DGFSSAWTVP	FASRlYVEMM
A. niger NRRL3135	NGIISILFAL	GLYNGTkPLS	TTTVENITQT	DGFSSAWTVP	FASRlYVEMM
A. fumigatus 13073	NSMVSIFFAL	GLYNGTEPLS	rTSVESaKEl	DGYSASWVVP	FGARAYFEtM
A. fumigatus 32722	NSMVSIFFAL	GLYNGTGPLS	rTSVESaKEl	DGYSASWVVP	FGARAYFEtM
A. fumigatus 58128	NSMVSIFFAL	GLYNGTEPLS	rTSVESaKEl	DGYSASWVVP	FGARAYFEtM
A. fumigatus 26906	NSMVSIFFAL	GLYNGTEPLS	rTSVESaKEl	DGYSASWVVP	FGARAYFEtM
A. fumigatus 32239	NGMIPIPFFAM	GLYNGTEPLS	qTSeESTKES	NGYSASWAVP	FGARAYFEtM
E. nidulans	NSMISIFFAM	GLYNGTQPLS	mDSVESIQEm	DGYAASWTVP	FGARAYFELM
T. thermophilus	NTMTSIFaAL	GLYNGTAkLS	TTEIKSIEET	DGYSAAWTVP	FGGRAYIEMM
M. thermophila	NDMMGVLgAL	GaYDGVPPLD	KTArrDpEEl	GGYAASWAVP	FAARiYVEKM
Consensus	NSMISIFFAL	GLYNGTAPLS	TTSVESIEET	DGYAASWTVP	FGARAYVEMM
Consensus phytase	**NSMISIFFAL**	**GLYNGTAPLS**	**TTSVESIEET**	**DGYSASWTVP**	**FGARAYVEMM**

	401				450
A. terreus 9A-1	QC........	.....RAEKE	PLVRVLVNDR	VMPLHGCPTD	KLGRCKrDAF
A. terreus cbs	QC........	.....RAEKQ	PLVRVLVNDR	VMPLHGCAVD	NLGRCKrDDF
A. niger var. *awamori*	QC........	.....QAEQE	PLVRVLVNDR	VVPLHGCPID	aLGRCTrDSF
A. niger T213	QC........	.....QAEQE	PLVRVLVNDR	VVPLHGCPID	aLGRCTrDSF
A. niger NRRL3135	QC........	.....QAEQE	PLVRVLVNDR	VVPLHGCPVD	aLGRCTrDSF
A. fumigatus 13073	QC........	.....KSEKE	PLVRALINDR	VVPLHGCDVD	KLGRCKLNDF
A. fumigatus 32722	QC........	.....KSEKE	PLVRALINDR	VVPLHGCDVD	KLGRCKLNDF
A. fumigatus 58128	QC........	.....KSEKE	SLVRALINDR	VVPLHGCDVD	KLGRCKLNDF
A. fumigatus 26906	QC........	.....KSEKE	PLVRALINDR	VVPLHGCDVD	KLGRCKLNDF
A. fumigatus 32239	QC........	.....KSEKE	PLVRALINDR	VVPLHGCAVD	KLGRCKLKDF
E. nidulans	QC........	.....E.KKE	PLVRVLVNDR	VVPLHGCAVD	KFGRCTLDDW
T. thermophilus	QC........	.....DDSDE	PVVRVLVNDR	VVPLHGCEVD	SLGRCKrDDF
M. thermophila	RCsggggggg	ggegrQEKDE	eMVRVLVNDR	VMTLkGCGAD	ErGMCTLErF
Consensus	QC--------	-----QAEKE	PLVRVLVNDR	VVPLHGCAVD	KLGRCKLDDF
Consensus phytase	**QC........**	**.....QAEKE**	**PLVRVLVNDR**	**VVPLHGCAVD**	**KLGRCKRDDF**

Fig. 1c

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

	451 471
A. terreus 9A-1	VAGLSFAQAG GNWADCF~~~ ~
A. terreus cbs	VEGLSFARAG NWAECF~~~
A. niger var. *awamori*	VrGLSFARSG GDWAECsA~~ ~
A. niger T213	VrGLSFARSG GDWAECFA~~ ~
A. niger NRRL3135	VrGLSFARSG DWAECFA~~
A. fumigatus 13073	VKGLSWARSG GNWGECFS~~ ~
A. fumigatus 32722	VKGLSWARSG GNWGECFS~~ ~
A. fumigatus 58128	VKGLSWARSG GNWGECFS~~ ~
A. fumigatus 26906	VKGLSWARSG GNWGECFS~~ ~
A. fumigatus 32239	VKGLSWARSG NSEQSFS~~
E. nidulans	VEGLNFARSG GNWkTCFTl~ ~
T. thermophilus	VrGLSFARqG GNWEGCYAas e
M. thermophila	IESMAFARGN GKWDlCFA~~ ~
Consensus	VEGLSFARSG GNWAECFA-- -
Consensus phytase	**VEGLSFARSG GNWAECFA.. .**

Fig. 1d

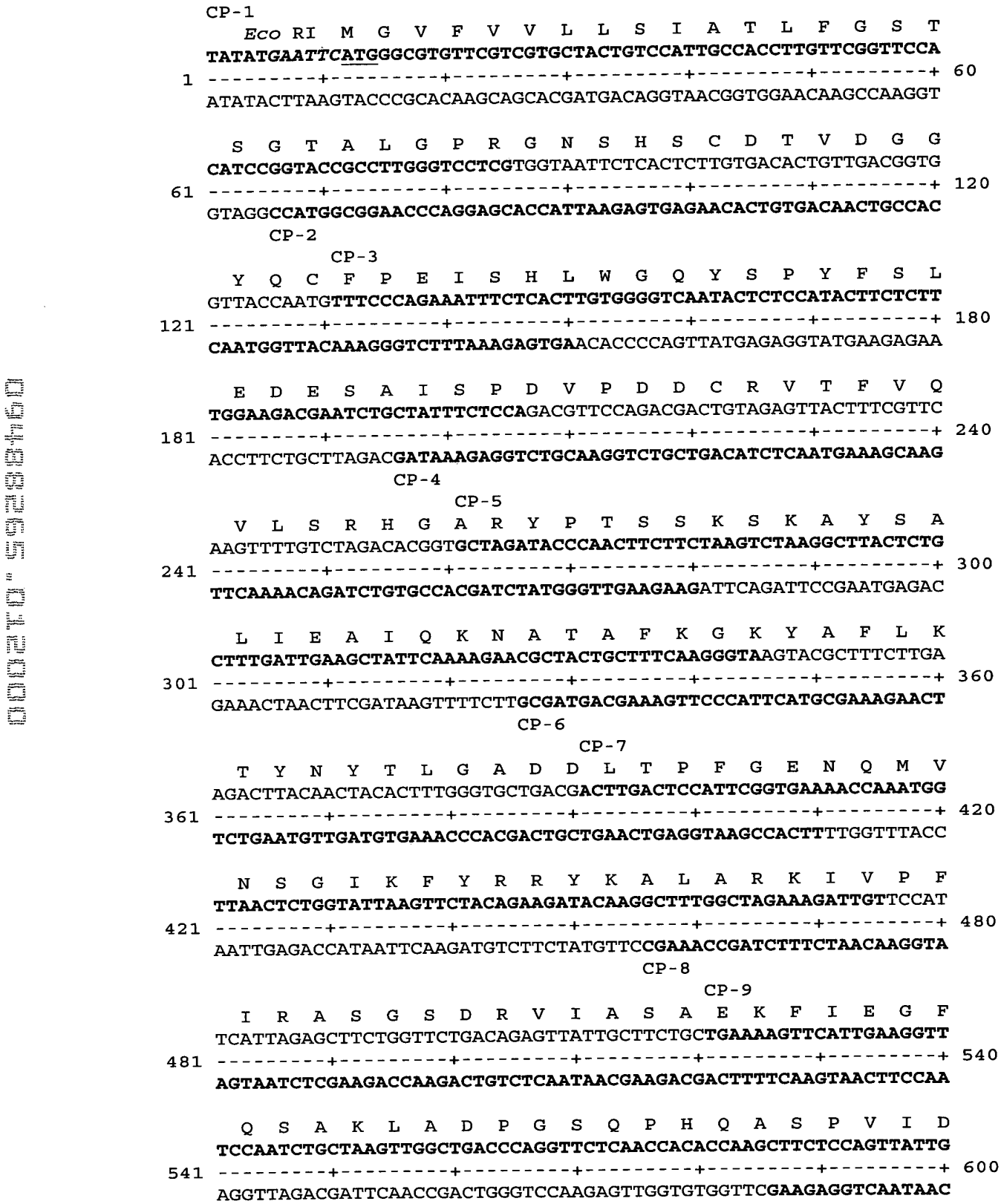


Fig. 2a

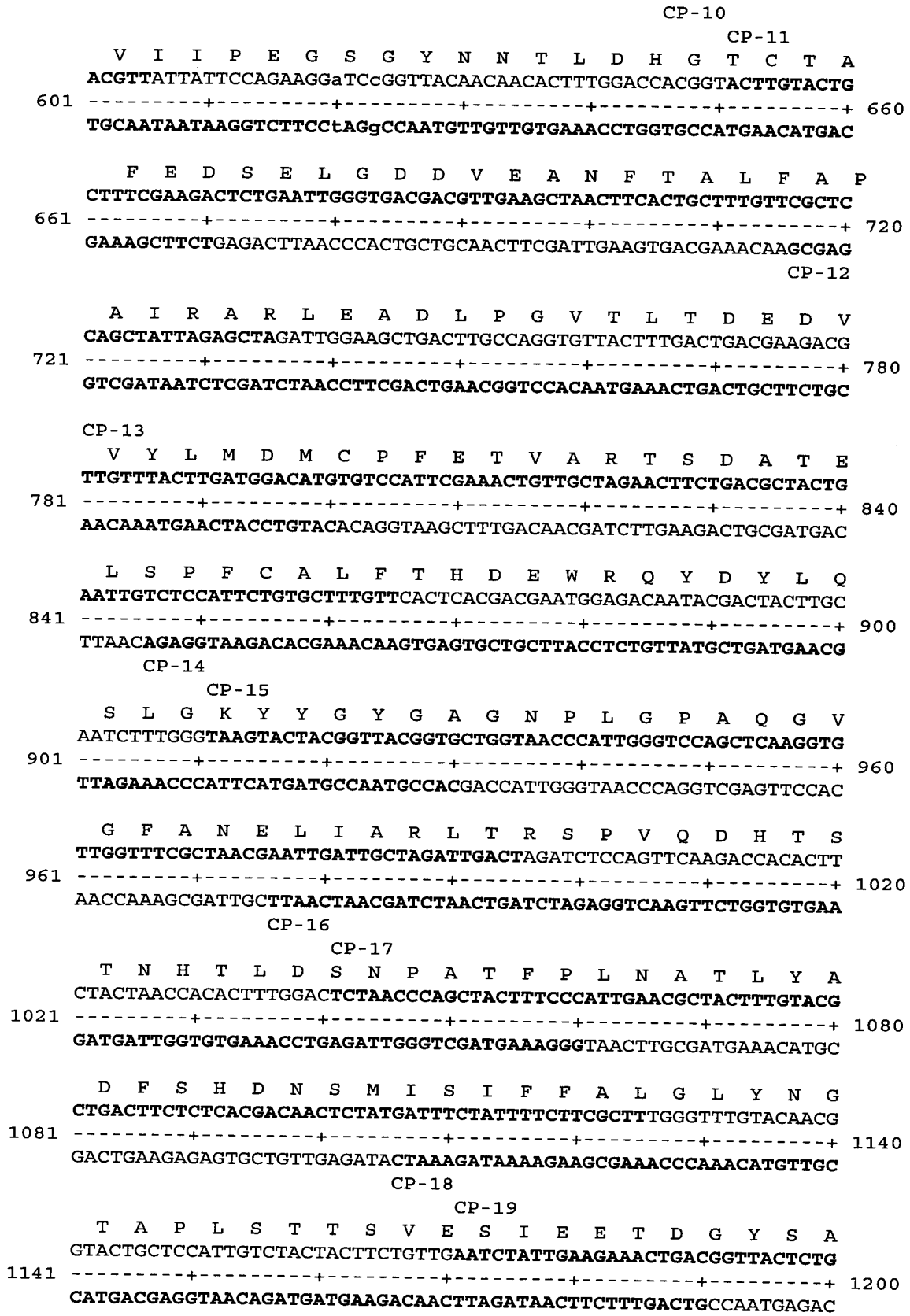


Fig. 2b

S W T V P F G A R A Y V E M M Q C Q A E
CTTCTTGGACTGTTCCATTCGGTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTG
1201 ---------+---------+---------+---------+---------+---------+ 1260
GAAGAACCTGACAAGGTAAGCCACGATCTCGAATG**CAACTTTACTACGTTACAGTTCGAC**
CP-20

CP-21
K E P L V R V L V N D R V V P L H G C A
AAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGT**TGTTCCATTGCACGGTTGTG**
1261 ---------+---------+---------+---------+---------+---------+ 1320
TTTTCCTTGGTAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC

V D K L G R C K R D D F V E G L S F A R
CTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTA
1321 ---------+---------+---------+---------+---------+---------+ 1380
GACAACTGTTCAACCCATCTACATTCTCTCTGCTGAAGCAACTTC**CAAACAGAAAGCGAT**
CP-22

S G G N W A E C F A * *Eco* RI
GATCTGGTGGTAACTGGGCTGAATGTTTCGCT*TAA*GAATTCATATA
1381 ---------+---------+---------+---------+------ 1426
CTAGACCACCATTGACCCGACTTACAAAGCGAATTCTTAAGTATAT

Fig. 2c

	1				50
P. involutus (*phyA1*)	SvP.KnTAPt	FPIPeseQrn	WSPYSPYFPL	AeYkAPPAGC	QInQVNIIQR
P. involutus (*phyA2*)	SvP.RniAPK	FSIPeseQrn	WSPYSPYFPL	AeYkAPPAGC	EInQVNIIQR
T. pubescens	hiPlRdTSAc	LdVTrDvQqs	WSmYSPYFPa	AtYvAPPASC	QInQVHIIQR
A. pediades	GgvvQaTfvQ	pfFPpQiQds	WAAYTPYYPV	qaYtPPPkDC	KItQVNIIQR
P. lycii	StQfsfvAAQ	LPIPaQntsn	WGPYdPFFPV	EpYaAPPEGC	tVtQVNLIQR
Basidio	**S-P-R-TAAQ**	**LPIP-Q-Q--**	**WSPYSPYFPV**	**A-Y-APPAGC**	**QI-QVNIIQR**

	51				100
P. involutus (*phyA1*)	HGARFPTSGA	TTRIKAGLTK	LQGvqnfTDA	KFNFIkSfkY	dLGnsDLVPF
P. involutus (*phyA2*)	HGARFPTSGA	ATRIKAGLSK	LQSvqnfTDP	KFDFIkSfTY	dLGtsDLVPF
T. pubescens	HGARFPTSGA	AkRIQTAVAK	LKAAsnyTDP	lLAFVtNyTY	sLGqDsLVeL
A. pediades	HGARFPTSGA	GTRIQAAVkK	LQSAktyTDP	RLDFLtNyTY	tLGhDDLVPF
P. lycii	HGARWPTSGA	rSRqvAAVAK	IQmArpfTDP	KYEFLnDfvY	kFGvADLLPF
Basidio	**HGARFPTSGA**	**ATRIQAAVAK**	**LQSA---TDP**	**KLDFL-N-TY**	**-LG-DDLVPF**

	101				150
P. involutus (*phyA1*)	GAaQSfDAGQ	EAFARYSkLV	SkNNLPFIRA	dGSDRVVDSA	TNWTAGFAsA
P. involutus (*phyA2*)	GAaQSfDAGl	EvFARYSkLV	SsDNLPFIRS	dGSDRVVDTA	TNWTAGFAsA
T. pubescens	GAtQSSEAGQ	EAFTRYSsLV	SaDELPFVRA	SGSDRVVATA	nNWTAGFAlA
A. pediades	GAlQSSQAGE	ETFqRYSfLV	SkENLPFVRA	SSSNRVVDSA	TNWTEGFSaA
P. lycii	GAnQShQTGt	DmYTRYStLf	egGDVPFVRA	AGdQRVVDSS	TNWTAGFGdA
Basidio	**GA-QSSQAGQ**	**EAFTRYS-LV**	**S-DNLPFVRA**	**SGSDRVVDSA**	**TNWTAGFA-A**

	151				200
P. involutus (*phyA1*)	ShNTvqPkLn	LILPQtGNDT	LEDNMCPaAG	DSDPQvNaWL	AVafPSITAR
P. involutus (*phyA2*)	SrNAiqPkLd	LILPQtGNDT	LEDNMCPaAG	ESDPQvDaWL	AsafPSVTAQ
T. pubescens	SsNSitPvLs	VIISEaGNDT	LDDNMCPaAG	DSDPQvNqWL	AqFAPPMTAR
A. pediades	ShHvlnPiLf	VILSEslNDT	LDDaMCPnAG	sSDPQtGiWt	SIYGTPIAnR
P. lycii	SgETvlPtLq	VVLqEeGNcT	LcNNMCPnEv	DGDest.tWL	GVFAPnITAR
Basidio	**S-NT--P-L-**	**VILSE-GNDT**	**LDDNMCP-AG**	**DSDPQ-N-WL**	**AVFAPPITAR**

	201				250
P. involutus (*phyA1*)	LNAAAPSvNL	TDtDAfNLvs	LCAFlTVSkE	kkSdFCtLFE	giPGsFeAFa
P. involutus (*phyA2*)	LNAAAPGANL	TDaDAfNLvs	LCPFmTVSkE	qkSdFCtLFE	giPGsFeAFa
T. pubescens	LNAGAPGANL	TDtDTyNLlt	LCPFETVAtE	rrSeFCDIYE	elQAE.dAFa
A. pediades	LNqqAPGANI	TAaDvsNLip	LCAFETIvkE	tpSpFCNLF.	.tPEEFaqFe
P. lycii	LNAAAPSANL	SDsDAltLmd	MCPFDTLSsG	naSpFCDLF.	.tAEEYvSYe
Basidio	**LNAAAPGANL**	**TD-DA-NL--**	**LCPFETVS-E**	**--S-FCDLFE**	**--PEEF-AF-**

Fig. 3a

	251				300
P. involutus (*phyA1*)	YgGDLDKFYG	TGYGQeLGPV	QGVGYVNELI	ARLTnsAVRD	NTQTNRTLDA
P. involutus (*phyA2*)	YaGDLDKFYG	TGYGQALGPV	QGVGYINELL	ARLTnsAVnD	NTQTNRTLDA
T. pubescens	YnADLDKFYG	TGYGQPLGPV	QGVGYINELI	ARLTaQnVsD	HTQTNsTLDS
A. pediades	YfGDLDKFYG	TGYGQPLGPV	QGVGYINELL	ARLTemPVRD	NTQTNRTLDS
P. lycii	YyyDLDKYYG	TGpGNALGPV	QGVGYVNELL	ARLTgQAVRD	ETQTNRTLDS
Basidio	**Y-GDLDKFYG**	**TGYGQPLGPV**	**QGVGYINELL**	**ARLT-QAVRD**	**NTQTNRTLDS**

	301				350
P. involutus (*phyA1*)	SPvTFPLNKT	FYADFSHDNl	MVAVFSAMGL	FrQPAPLsTS	vPNPwRTWrT
P. involutus (*phyA2*)	APdTFPLNKT	MYADFSHDNl	MVAVFSAMGL	FrQSAPLsTS	tPDPNRTWLT
T. pubescens	SPeTFPLNRT	LYADFSHDNQ	MVAIFSAMGL	FNQSAPLDPT	tPDPaRTFLv
A. pediades	SPlTFPLDRS	IYADLSHDNQ	MIAIFSAMGL	FNQSSPLDPS	fPNPKRTWVT
P. lycii	dPaTFPLNRT	FYADFSHDNt	MVPIFAALGL	FNaTA.LDPl	kPDeNRlWVd
Basidio	**SP-TFPLNRT**	**FYADFSHDNQ**	**MVAIFSAMGL**	**FNQSAPLDPS**	**-PDPNRTWVT**

	351				400
P. involutus (*phyA1*)	SsLVPFSGRM	VVERLsC..f	GT........	.......tkV	RVLVQDqVQP
P. involutus (*phyA2*)	SsVVPFSARM	aVERLsC..a	GT........	.......tkV	RVLVQDqVQP
T. pubescens	kKIVPFSARM	VVERLdC..g	GA........	.......qsV	RLLVNDAVQP
A. pediades	SRLtPFSARM	VtERLlCqrd	GTgsggpsri	mrngnvqtfV	RILVNDALQP
P. lycii	SKLVPFSGHM	tVEKLaC...	....	....sgkeaV	RVLVNDAVQP
Basidio	**SKLVPFSARM**	**VVERL-C---**	**GT--------**	**---------V**	**RVLVNDAVQP**

	401			441	
P. involutus (*phyA1*)	LEFCGGDrNG	lCTLAkFVES	QtFARsDGaG	DFEKCFATSa	~
P. involutus (*phyA2*)	LEFCGGDqDG	lCALDkFVES	QaYARsGGaG	DFEKCLATTv	~
T. pubescens	LAFCGADtsG	vCTLDAFVES	QaYARNDGEG	DFEKCFAT~~	~
A. pediades	LKFCGGDmDS	lCTLEAFVES	QkYAREDGQG	DFEKCFD~~~	~
P. lycii	LEFCGG.vDG	vCeLsAFVES	QtYARENGQG	DFAKCgfvPs	e
Basidio	**LEFCGGD-DG**	**-CTLDAFVES**	**Q-YAREDGQG**	**DFEKCFATP-**	**-**

Fig. 3b

	1				50
A. terreus 9a1	KhsdCNSVDh	GYQCfPELSH	kWGlYAPYFS	LqDESPFPlD	VPeDCHITFV
A. terreus cbs	NhsdCtSVDr	GYQCfPELSH	kWGlYAPYFS	LqDESPFPlD	VPdDCHITFV
A. niger var. *awamori*	NqsTCDTVDq	GYQCfSEtSH	LWGQYAPFFS	LANESAISPD	VPaGCRVTFa
A. niger NRRL3135	NqsSCDTVDq	GYQCfSEtSH	LWGQYAPFFS	LANESvISPE	VPaGCRVTFa
A. fumigatus 13073	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPkDCRITLV
A. fumigatus 32722	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPkDCRITLV
A. fumigatus 58128	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPkDCRITLV
A. fumigatus 26906	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPkDCRITLV
A. fumigatus 32239	GSkACDTVEl	GYQCsPGtSH	LWGQYSPFFS	LEDElSVSSD	LPkDCRVTFV
E. nidulans	QNHSCNTaDG	GYQCfPNVSH	VWGQYSPYFS	IEQESAISeD	VPhGCeVTFV
T. thermophilus	DSHSCNTVEG	GYQCrPEISH	sWGQYSPFFS	LADQSEISPD	VPqNCKITFV
T. lanuginosus	~~~~~~~~~~	~~~~nvDIAR	hWGQYSPFFS	LAEvSEISPA	VPkGCRVeFV
M. thermophila	ESRPCDTpDl	GFQCgTAISH	FWGQYSPYFS	VPsElDaS..	IPdDCeVTFa
Basidio	xSxPxrxtAA	qLPipxQxqx	xWSPYSPYFP	VAxyxA....	pPaGCQIxqV
Consensus	NSHSCDTVDG	GYQC-PEISH	LWGQYSPFFS	LADESAISPD	VP-GCRVTFV
Fcp10	**NSHSCDTVDG**	**GYQCFPEISH**	**LWGQYSPFFS**	**LADESAISPD**	**VPKGCRVTFV**

	51				100
A. terreus 9a1	QVLARHGARs	PThSKTKaYA	AtIaAIQKSA	TaFpGKYAFL	QSYNYSLDSE
A. terreus cbs	QVLARHGARs	PTdSKTKaYA	AtIaAIQKNA	TaLpGKYAFL	KSYNYSMGSE
A. niger var. *awamori*	QVLSRHGARY	PTeSKGKKYS	ALIeEIQQNv	TtFDGKYAFL	KTYNYSLGAD
A. niger NRRL3135	QVLSRHGARY	PTdSKGKKYS	ALIeEIQQNA	TtFDGKYAFL	KTYNYSLGAD
A. fumigatus 13073	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 32722	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 58128	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 26906	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus 32239	QVLSRHGARY	PTASKSKKYk	kLVtAIQKNA	TeFKGKFAFL	ETYNYTLGAD
E. nidulans	QVLSRHGARY	PTeSKSKaYS	GLIeAIQKNA	TsFwGQYAFL	ESYNYTLGAD
T. thermophilus	QLLSRHGARY	PTSSKTElYS	qLIsrIQKtA	TaYKGyYAFL	KdYrYqLGAN
T. lanuginosus	QVLSRHGARY	PTAhKSEvYA	ELLqrIQDtA	TeFKGDFAFL	RdYaYhLGAD
M. thermophila	QVLSRHGARa	PTlkRAasYv	DLIdrIHhGA	isYgPgYEFL	RTYDYTLGAD
Basidio	NIIqRHGARF	PTSGaAtRiq	AaVakLQsax	xxtDPKLDFL	xnxtYxLGxD
Consensus	QVLSRHGARY	PTSSKSKKYS	ALI-AIQKNA	T-FKGKYAFL	KTYNYTLGAD
Fcp10	**QVLSRHGARY**	**PTSSKSKKYS**	**ALIEAIQKNA**	**TAFKGKYAFL**	**KTYNYTLGAD**

	101				150
A. terreus 9a1	ELTPFGrNQL	rDlGaQFYeR	YNAL.TRhIn	PFVRATDAsR	VhESAEKFVE
A. terreus cbs	NLTPFGrNQL	qDlGaQFYRR	YDTL.TRhIn	PFVRAADSsR	VhESAEKFVE
A. niger var. *awamori*	DLTPFGEQEL	VNSGIKFYQR	YESL.TRnII	PFIRSSGSsR	VIASGEKFIE
A. niger NRRL3135	DLTPFGEQEL	VNSGIKFYQR	YESL.TRnIV	PFIRSSGSsR	VIASGKKFIE
A. fumigatus 13073	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARsVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus 32722	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARsVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus 58128	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARsVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus 26906	DLTAFGEQQL	VNSGIKFYQR	YKAL.ARsVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus 32239	DLTPFGEQQM	VNSGIKFYQK	YKAL.AgsVV	PFIRSSGSDR	VIASGEKFIE
E. nidulans	DLTiFGENQM	VDSGaKFYRR	YKnL.ARknt	PFIRASGSDR	VVASAEKFIN
T. thermophilus	DLTPFGENQM	IQlGIKFYnH	YKSL.ARnaV	PFVRCSGSDR	VIASGrlFIE
T. lanuginosus	NLTRFGEEQM	MESGrQFYHR	YREq.AReIV	PFVRAAGSAR	VIASAEfFnr
M. thermophila	ELTRtGQQQM	VNSGIKFYRR	YRAL.ARksI	PFVRTAGqDR	VVhSAENFtQ
Basidio	DLvPFGAxQs	sQAGqEaFtR	YsxLvSxdnL	PFVRASGSDR	VVDSAtNWtA
Consensus	DLTPFGEQQM	VNSGIKFYRR	YKAL-AR-IV	PFVRASGSDR	VIASAEKFIE
Fcp10	**DLTPFGEQQM**	**VNSGIKFYRR**	**YKAL.ARKIV**	**PFVRASGSDR**	**VIASAEKFIE**

Fig. 4a

	151				200
A. terreus 9a1	GFQTARqDDh	hAnphQPSPr	VDVaIPEGsA	YNNTLEHSLC	TAFEs...St
A. terreus cbs	GFQNARqGDP	hAnphQPSPr	VDVVIPEGtA	YNNTLEHSIC	TAFEa...St
A. niger var. awamori	GFQSTKLkDP	rAqpgQSSPk	IDVVISEAsS	sNNTLDpGtC	TvFEd...SE
A. niger NRRL3135	GFQSTKLkDP	rAqpgQSSPk	IDVVISEAsS	sNNTLDpGtC	TvFEd...SE
A. fumigatus 13073	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEa...SQ
A. fumigatus 32722	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEa...SQ
A. fumigatus 58128	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEa...SQ
A. fumigatus 26906	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEa...SQ
A. fumigatus 32239	GFQqANVADP	gAt.nRAAPV	ISVIIPESeT	YNNTLDHSVC	TnFEa...SE
E. nidulans	GFRkAQLhDh	g.s.gQATPV	VNVIIPEidG	FNNTLDHStC	vSFEn...dE
T. thermophilus	GFQSAKVlDP	hSdkhDAPPt	INVIIeEGpS	YNNTLDtGsC	PvFEd...Ss
T. lanuginosus	GFQdAKdrDP	rSnkdQAePV	INVIISEEtG	sNNTLDgltC	PAaEe...Ap
M. thermophila	GFHSAlLADR	gStvrPTlPy	dmVVIPETaG	aNNTLHNDLC	TAFEegPySt
Basidio	GFaxA.....	..sxntxxPx	LxVILSExg.	.NDTLDDNMC	......PxAG
Consensus	GFQSAKLADP	-A---QASPV	INVIIPEG-G	YNNTLDHGLC	TAFE--P-SE
Fcp10	**GFQSAKLADP**	**GANPHQASPV**	**INVIIPEGAG**	**YNNTLDHGLC**	**TAFEE...SE**

	201				250
A. terreus 9a1	VGDDavANFT	AVFAPAIaqR	LEAdLPGVQL	StDDVVNLMA	MCPFETVSlT
A. terreus cbs	VGDAaADNFT	AVFAPAIakR	LEAdLPGVQL	SADDVVNLMA	MCPFETVSlT
A. niger var. awamori	LADtVEANFT	AtFAPSIRqR	LEndLSGVtL	TDtEVtyLMD	MCSFDTIStS
A. niger NRRL3135	LADtVEANFT	AtFvPSIRqR	LEndLSGVtL	TDtEVtyLMD	MCSFDTIStS
A. fumigatus 13073	LGDEVAANFT	ALFAPdIRAR	aEkhLPGVtL	TDEDVVSLMD	MCSFDTVArT
A. fumigatus 32722	LGDEVAANFT	ALFAPdIRAR	aEkhLPGVtL	TDEDVVSLMD	MCSFDTVArT
A. fumigatus 58128	LGDEVAANFT	ALFAPdIRAR	aEkhLPGVtL	TDEDVVSLMD	MCSFDTVArT
A. fumigatus 26906	LGDEVAANFT	ALFAPdIRAR	aKkhLPGVtL	TDEDVVSLMD	MCSFDTVArT
A. fumigatus 32239	LGDEVEANFT	ALFAPAIRAR	IEkhLPGVQL	TDDDVVSLMD	MCSFDTVArT
E. nidulans	rADEIEANFT	AIMGPPIRkR	LEndLPGIKL	TNENVIyLMD	MCSFDTMArT
T. thermophilus	gGHDaQEKFA	kqFAPAIlEK	IKDhLPGVDL	AvsDVpyLMD	LCPFETLArn
T. lanuginosus	.DptqpAEFl	qVFGPRVlkK	ItkhMPGVNL	TlEDVplFMD	LCPFDTVGsd
M. thermophila	IGDDaQDtYl	StFAGPItAR	VNAnLPGaNL	TDADtVaLMD	LCPFETVAsS
Basidio	dSDpqxnxWl	AVFAPPItAR	LNAaaPGaNL	TDxDaxNLxx	LCPFETVS..
Consensus	LGDDVEANFT	AVFAPPIRAR	LEA-LPGVNL	TDEDVVNLMD	MCPFDTVA-T
Fcp10	**LGDDVEANFT**	**AVFAPPIRAR**	**LEAHLPGVNL**	**TDEDVVNLMD**	**MCPFDTVART**

	251				300
A. terreus 9a1	dD..Aht...	......LSPF	CDLFTa..tE	WtQYNYLlSL	dKYYGYGGGN
A. terreus cbs	dD..Aht...	......LSPF	CDLFTa..aE	WtQYNYLlSL	dKYYGYGGGN
A. niger var. awamori	Tv..DTK...	......LSPF	CDLFTH..dE	WiHYDYLQSL	kKYYGHGAGN
A. niger NRRL3135	Tv..DTK...	......LSPF	CDLFTH..dE	WiNYDYLQSL	kKYYGHGAGN
A. fumigatus 13073	SD..ASQ...	......LSPF	CQLFTH..nE	WkKYNYLQSL	gKYYGYGAGN
A. fumigatus 32722	SD..ASQ...	......LSPF	CQLFTH..nE	WkKYNYLQSL	gKYYGYGAGN
A. fumigatus 58128	SD..ASQ...	......LSPF	CQLFTH..nE	WkKYNYLQSL	gKYYGYGAGN
A. fumigatus 26906	SD..ASQ...	......LSPF	CQLFTH..nE	WkKYNYLQSL	gKYYGYGAGN
A. fumigatus 32239	AD..ASE...	......LSPF	CAIFTH..nE	WkKYDYLQSL	gKYYGYGAGN
E. nidulans	AH..GTE...	......LSPF	CAIFTE..kE	WlQYDYLQSL	sKYYGYGAGS
T. thermophilus	ht..DT....	......LSPF	CALsTQ..eE	WqaYDYYQSL	gKYYGnGGGN
T. lanuginosus	PvlfPrQ...	......LSPF	CHLFTa..dD	WmaYDYYyTL	dKYYSHGGGS
M. thermophila	SsdpATadag	ggngrpLSPF	CrLFSE..sE	WraYDYLQSV	gKWYGYGPGN
Basidio	....	...xexxSxF	CDLFexxpeE	FxaFxYxgdL	dKFYGtGyGQ
Consensus	SD--ATQ---	------LSPF	CDLFTH---E	W-QYDYLQSL	-KYYGYGAGN
Fcp10	**SD..ATQ...**	**......LSPF**	**CDLFTH..DE**	**WIQYDYLQSL**	**GKYYGYGAGN**

Fig. 4b

	301				350
A. terreus 9a1	PLGPvQGVGW	aNELMARLTR	A.PVHDHTCv	NNTLDASPAT	FPLNATLYAD
A. terreus cbs	PLGPvQGVGW	aNELIARLTR	S.PVHDHTCv	NNTLDANPAT	FPLNATLYAD
A. niger var. *awamori*	PLGPTQGVGY	aNELIARLTH	S.PVHDDTSS	NHTLDSNPAT	FPLNSTLYAD
A. niger NRRL3135	PLGPTQGVGY	aNELIARLTH	S.PVHDDTSS	NHTLDSSPAT	FPLNSTLYAD
A. fumigatus 13073	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST	NsTLvSNPAT	FPLNATMYvD
A. fumigatus 32722	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST	NsTLvSNPAT	FPLNATMYvD
A. fumigatus 58128	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST	NsTLvSNPAT	FPLNATMYvD
A. fumigatus 26906	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST	NsTLvSNPAT	FPLNATMYvD
A. fumigatus 32239	PLGPAQGIGF	tNELIARLTN	S.PVQDHTST	NsTLDSDPAT	FPLNATIYvD
E. nidulans	PLGPAQGIGF	tNELIARLTQ	S.PVQDNTST	NHTLDSNPAT	FPLDrkLYAD
T. thermophilus	PLGPAQGVGF	vNELIARMTH	S.PVQDYTTv	NHTLDSNPAT	FPLNATLYAD
T. lanuginosus	AFGPSRGVGF	vNELIARMTg	NlPVKDHTTv	NHTLDdNPET	FPLDAvLYAD
M. thermophila	PLGPTQGVGF	vNELLARLA.	GvPVRDgTST	NRTLDGDPrT	FPLGrPLYAD
Basidio	PLGPvQGVGY	iNELLARLTx	qa.VRDNTqT	NRTLDSSPxT	FPLNrTFYAD
Consensus	PLGPAQGVGF	-NELIARLTH	S-PVQDHTST	NHTLDSNPAT	FPLNATLYAD
Fcp10	**PLGPAQGVGF**	**VNELIARLTH**	**S.PVQDHTST**	**NHTLDSNPAT**	**FPLNATLYAD**

	351				400
A. terreus 9a1	FSHDSnLVSI	FWALGLYNGT	aPLSqTSVE.	.SvsQTDGYA	AAWTVPFAAR
A. terreus cbs	FSHDSnLVSI	FWALGLYNGT	kPLSqTTVE.	.ditrTDGYA	AAWTVPFAAR
A. niger var. *awamori*	FSHDNGIISI	LFALGLYNGT	kPLSTTTVE.	.NitQTDGFS	SAWTVPFASR
A. niger NRRL3135	FSHDNGIISI	LFALGLYNGT	kPLSTTTVE.	.NitQTDGFS	SAWTVPFASR
A. fumigatus 13073	FSHDNSMVSI	FFALGLYNGT	ePLSrTSVE.	.SaKElDGYS	ASWvVPFGAR
A. fumigatus 32722	FSHDNSMVSI	FFALGLYNGT	gPLSrTSVE.	.SaKElDGYS	ASWvVPFGAR
A. fumigatus 58128	FSHDNSMVSI	FFALGLYNGT	ePLSrTSVE.	.SaKElDGYS	ASWvVPFGAR
A. fumigatus 26906	FSHDNSMVSI	FFALGLYNGT	ePLSrTSVE.	.SaKElDGYS	ASWvVPFGAR
A. fumigatus 32239	FSHDNGMIPI	FFAMGLYNGT	ePLSqTSeE.	.StKESNGYS	ASWAVPFGAR
E. nidulans	FSHDNSMISI	FFAMGLYNGT	qPLSmdSVE.	.SiQEmDGYA	ASWTVPFGAR
T. thermophilus	FSHDNTMtSI	FaALGLYNGT	akLSTTeIK.	.SiEETDGYS	AAWTVPFGGR
T. lanuginosus	FSHDNTMtGI	FsAMGLYNGT	kPLSTSkIQP	pTgAAADGYA	ASWTVPFAAR
M. thermophila	FSHDNdMMGV	LgALGaYDGv	pPLdkTA..R	rdpEElGGYA	ASWAVPFAAR
Basidio	FSHDNqMVAI	FsAMGLFNqS	aPLdPSxpDP	nrt.....Wv	TSklVPFSAR
Consensus	FSHDNTMVSI	FFALGLYNGT	-PLSTTSVEP	-S-EETDGYA	ASWTVPFAAR
Fcp10	**FSHDNTMVSI**	**FFALGLYNGT**	**KPLSTTSVE.**	**.SIEETDGYA**	**ASWTVPFAAR**

	401				450
A. terreus 9a1	AYVEMMQC..	ra........	.....EKEPL	VRVLVNDRVM	PLHGCPtDKL
A. terreus cbs	AYIEMMQC..	ra........	.....EKQPL	VRVLVNDRVM	PLHGCAVDNL
A. niger var. *awamori*	lYVEMMQC..	Qa........	.....EQEPL	VRVLVNDRVV	PLHGCPIDaL
A. niger NRRL3135	lYVEMMQC..	Qa........	.....EQEPL	VRVLVNDRVV	PLHGCPVDaL
A. fumigatus 13073	AYfEtMQC..	Ks........	.....EKEPL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus 32722	AYfEtMQC..	Ks........	.....EKEPL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus 58128	AYfEtMQC..	Ks........	.....EKESL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus 26906	AYfEtMQC..	Ks........	.....EKEPL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus 32239	AYfEtMQC..	Ks........	.....EKEPL	VRaLINDRVV	PLHGCAVDKL
E. nidulans	AYfELMQC..	E.........	.....KKEPL	VRVLVNDRVV	PLHGCAVDKF
T. thermophilus	AYIEMMQC..	Dd........	.....sDEPV	VRVLVNDRVV	PLHGCEVDsL
T. lanuginosus	AYVELLRC..	Etetsseeee	EG...EDEPF	VRVLVNDRVV	PLHGCrVDRW
M. thermophila	iYVEkMRC..	sgggggggg	EGrqeKDEeM	VRVLVNDRVM	TLkGCGaDEr
Basidio	mvVErLxCxx	xgtxxxxxxx	xxxxxxxxxx	VRVLVNDaVq	PLEfCGgDxd
Consensus	AYVEMMQC--	E---------	EG---EKEPL	VRVLVNDRVV	PLHGCGVDKL
Fcp10	**AYVEMMQC..**	**EA........**	**.....EKEPL**	**VRVLVNDRVV**	**PLHGCGVDKL**

Fig. 4c

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

	451		482
A. terreus 9a1	GRCKrDAFVA	GLSFAQAG..	GNWADCF~~~ ~~
A. terreus cbs	GRCKrDDFVE	GLSFARAG..	GNWAECF~~~ ~~
A. niger var. *awamori*	GRCtrDsFVr	GLSFARSG..	GDWAECsA~~ ~~
A. niger NRRL3135	GRCtrDsFVr	GLSFARSG..	GDWAECFA~~ ~~
A. fumigatus 13073	GRCKlNDFVK	GLSWARSG..	GNWGECFS~~ ~~
A. fumigatus 32722	GRCKlNDFVK	GLSWARSG..	GNWGECFS~~ ~~
A. fumigatus 58128	GRCKlNDFVK	GLSWARSG..	GNWGECFS~~ ~~
A. fumigatus 26906	GRCKlNDFVK	GLSWARSG..	GNWGECFS~~ ~~
A. fumigatus 32239	GRCKlKDFVK	GLSWARSG..	GNSEQSFS~~ ~~
E. nidulans	GRCtlDDWVE	GLNFARSG..	GNWKtCFTl~ ~~
T. thermophilus	GRCKrDDFVr	GLSFARqG..	GNWEGCYAas e~
T. lanuginosus	GRCRrDEWIK	GLTFARqG..	GHWDrCF~~~ ~~
M. thermophila	GmCtlErFIE	SMAFARGN..	GKWDlCFA~~ ~~
Basidio	GxCtlDAFVE	SqxYAReDgq	GDFEKCFAtp xx
Consensus	GRCK-DDFVE	GLSFARSG--	GNWEECFA-- --
Fcp10	**GRCKRDDFVE**	**GLSFARSG..**	**GNWEECFA.. ..**

Fig. 4d

```
       CP-1
          Eco RI M   G   V   F   V   V   L   L   S   I   A   T   L   F   G   S   T   17
       TATATGAATTCATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCA
     1 ---------+---------+---------+---------+---------+---------+ 60
       ATATACTTAAGTACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGT

         S   G   T   A   L   G   P   R   G   N   S   H   S   C   D   T   V   D   G   G   37
       CATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTG
    61 ---------+---------+---------+---------+---------+---------+ 120
       GTAGGCCATGGCGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACTGCCAC
           CP-2
               CP-3.10
         Y   Q   C   F   P   E   I   S   H   L   W   G   Q   Y   S   P   F   F   S   L   57
       GTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTT
   121 ---------+---------+---------+---------+---------+---------+ 180
       CAATGGTTACAAAGGGTCTTTAAAGAGTGAACACCCCAGTTATGAGAGGTAAGAAGAGAA

         A   D   E   S   A   I   S   P   D   V   P   K   G   C   R   V   T   F   V   Q   77
       TGGCTGACGAATCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTC
   181 ---------+---------+---------+---------+---------+---------+ 240
       ACCGACTGCTTAGACGATAAAGAGGTCTGCAAGGTTTCCCGACATCTCAATGAAAGCAAG
                         CP-4.10
                            CP-5.10
         V   L   S   R   H   G   A   R   Y   P   T   S   S   K   S   K   K   Y   S   A   97
       AAGTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTG
   241 ---------+---------+---------+---------+---------+---------+ 300
       TTCAAAACAGATCTGTGCCACGATCTATGGGTTGAAGAAGATTCAGATTCTTCATGAGAC

         L   I   E   A   I   Q   K   N   A   T   A   F   K   G   K   Y   A   F   L   K  117
       CTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGA
   301 ---------+---------+---------+---------+---------+---------+ 360
       GAAACTAACTTCGATAAGTTTTCTTGCGATGACGAAAGTTCCCATTCATGCGAAAGAACT
                                                CP-6
                                                     CP-7.10
         T   Y   N   Y   T   L   G   A   D   D   L   T   P   F   G   E   Q   Q   M   V  137
       AGACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGG
   361 ---------+---------+---------+---------+---------+---------+ 420
       TCTGAATGTTGATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTGTTGTTTACC

         N   S   G   I   K   F   Y   R   R   Y   K   A   L   A   R   K   I   V   P   F  157
       TTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCAT
   421 ---------+---------+---------+---------+---------+---------+ 480
       AATTGAGACCATAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTA
                                                          CP-8.10
                                                              CP-9.10
         V   R   A   S   G   S   D   R   V   I   A   S   A   E   K   F   I   E   G   F  177
       TCGTTAGAGCTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTT
   481 ---------+---------+---------+---------+---------+---------+ 540
       AGCAATCTCGAAGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAA

         Q   S   A   K   L   A   D   P   G   A   N   P   H   Q   A   S   P   V   I   N  197
       TCCAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTA
   541 ---------+---------+---------+---------+---------+---------+ 600
       AGGTTAGACGATTCAACCGACTGGGTCCACGATTGGGTGTGGTTCGAAGAGGTCAATAAT
```

Fig. 5a

```
                                                        CP-10.10
                                                            CP-11.10
      V  I  I  P  E  G  A  G  Y  N  N  T  L  D  H  G  L  C  T  A 217
     ACGTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTG
 601 ---------+---------+---------+---------+---------+---------+ 660
     TGCAATAATAAGGTCTTCCACGACCAATGTTGTTGTGAAACCTGGTGCCAAACACATGAC

      F  E  E  S  E  L  G  D  D  V  E  A  N  F  T  A  V  F  A  P 237
     CTTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTC
 661 ---------+---------+---------+---------+---------+---------+ 720
     GAAAGCTTCTTAGACTTAACCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAG
                                                          CP-12.10

      P  I  R  A  R  L  E  A  H  L  P  G  V  N  L  T  D  E  D  V 257
     CACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACG
 721 ---------+---------+---------+---------+---------+---------+ 780
     GTGGATAATCTCGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGC

     CP-13.10
      V  N  L  M  D  M  C  P  F  D  T  V  A  R  T  S  D  A  T  Q 277
     TTGTTAACTTGATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTC
 781 ---------+---------+---------+---------+---------+---------+ 840
     AACAATTGAACTACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAG

      L  S  P  F  C  D  L  F  T  H  D  E  W  I  Q  Y  D  Y  L  Q 297
     AATTGTCTCCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGC
 841 ---------+---------+---------+---------+---------+---------+ 900
     TTAACAGAGGTAAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACG
           CP-14.10
               CP-15.10
      S  L  G  K  Y  Y  G  Y  G  A  G  N  P  L  G  P  A  Q  G  V 317
     AATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTG
 901 ---------+---------+---------+---------+---------+---------+ 960
     TTAGAAACCCATTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTCGAGTTCCAC

      G  F  V  N  E  L  I  A  R  L  T  H  S  P  V  Q  D  H  T  S 337
     TTGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTT
 961 ---------+---------+---------+---------+---------+---------+ 1020
     AACCAAAGCAATTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAA
                   CP-16.10
                      CP-17.10
      T  N  H  T  L  D  S  N  P  A  T  F  P  L  N  A  T  L  Y  A 357
     CTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACG
1021 ---------+---------+---------+---------+---------+---------+ 1080
     GATGATTGGTGTGAAACCTGAGATTGGGTCGATGAAAGGGTAACTTGCGATGAAACATGC

      D  F  S  H  D  N  T  M  V  S  I  F  F  A  L  G  L  Y  N  G 377
     CTGACTTCTCTCACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACG
1081 ---------+---------+---------+---------+---------+---------+ 1140
     GACTGAAGAGAGTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGC
                          CP-18.10
                              CP-19.10
      T  K  P  L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  A  A 397
     GTACTAAGCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTG
1141 ---------+---------+---------+---------+---------+---------+ 1200
     CATGATTCGGTAACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGCGAC
```

Fig. 5b

```
         S  W  T  V  P  F  A  A  R  A  Y  V  E  M  M  Q  C  E  A  E 417
       CTTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTG
  1201 ---------+---------+---------+---------+---------+---------+ 1260
       GAAGAACCTGACAAGGTAAGCCACGATCTCGAATGCAACTTTACTACGTTACACTTCGAC
                                                 CP-20.10
                                                      CP-21.10

         K  E  P  L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  G 437
       AAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTG
  1261 ---------+---------+---------+---------+---------+---------+ 1320
       TTTTCCTTGGTAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC

         V  D  K  L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R 457
       GTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTA
  1321 ---------+---------+---------+---------+---------+---------+ 1380
       CACAACTGTTCAACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGAT
                                                          CP-22.10
         S  G  G  N  W  E  E  C  F  A  *  Eco RI        467
       GATCTGGTGGTAACTGGGAAGAATGTTTCGCTTAAGAATTCATATA
  1381 ---------+---------+---------+---------+------ 1426
       CTAGACCACCATTGACCCTTCTTACAAAGCGAATTCTTAAGTATAT
```

Fig. 5c

	1				50
P. involutus (phyA1)	~~~~~~~~~~	~FPipeseqR	nWSPYSPYFP	LAEykA....	pPaGCQInqV
P. involutus (phyA2)	~~~~~~~~~~	~FsipeseqR	nWSPYSPYFP	LAEykA....	pPaGCeInqV
T. pubescens	~~~~~~~~~~	~LDvtRDVqQ	sWSmYSPYFP	aAtyvA....	pPaSCQInqV
A. pediades	~~~~~~~~~~	~pffpPQIqD	sWAaYTPYYP	VqAyTP....	pPKDCKITqV
P. lycii	~~~~~~~~~~	~LPipAQnTs	nWGPYdPFFP	VEpyAA....	pPEGCtVTqV
A. terreus 9a1	KhsdCNSVDh	GYQCfPELSH	kWGlYAPYFS	LqDESPFPlD	VPEDCHITFV
A. terreus cbs	NhsdCtSVDr	GYQCfPELSH	kWGlYAPYFS	LqDESPFPlD	VPDDCHITFV
A. niger var. *awamori*	NqsTCDTVDq	GYQCfSEtSH	LWGQYAPFFS	LANESAISPD	VPaGCRVTFa
A. niger T213	NqsSCDTVDq	GYQCfSEtSH	LWGQYAPFFS	LANESvISPD	VPaGCRVTFa
A. niger NRRL3135	NqsSCDTVDq	GYQCfSEtSH	LWGQYAPFFS	LANESvISPE	VPaGCRVTFa
A. fumigatus ATCC13073	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPKDCRITLV
A. fumigatus ATCC32722	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPKDCRITLV
A. fumigatus ATCC58128	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPKDCRITLV
A. fumigatus ATCC26906	GSkSCDTVDl	GYQCsPAtSH	LWGQYSPFFS	LEDElSVSSK	LPKDCRITLV
A. fumigatus ATCC32239	GSkACDTVEl	GYQCsPGtSH	LWGQYSPFFS	LEDElSVSSD	LPKDCRVTFV
E. nidulans	QNHSCNTaDg	GYQCfPNVSH	VWGQYSPYFS	IEQESAISeD	VPhGCeVTFV
T. thermophilus	DSHSCNTVEg	GYQCrPEISH	sWGQYSPFFS	LADQSEISPD	VPQNCKITFV
T. lanuginosus	~~~~~~~~~~	~~~~nvDIAR	hWGQYSPFFS	LAEvSEISPA	VPKGCRVeFV
M. thermophila	ESRPCDTpDl	GFQCgTAISH	FWGQYSPYFS	VPsElDaS..	IPDDCeVTFa
Consensus Seq. 11	**NSHSCDTVD-**	**GYQC-PEISH**	**LWGQYSPFFS**	**LADESAISPD**	**VPKGCRVTFV**

	51				100
P. involutus (phyA1)	NIIqRHGARF	PTSGaTtRik	AgLtKLQgvq	nftDAKFnFI	KSFKYdLGns
P. involutus (phyA2)	NIIqRHGARF	PTSGaAtRik	AgLsKLQsvq	nftDPKFDFI	KSFtYdLGTs
T. pubescens	HIIqRHGARF	PTSGaAKRiq	TaVAKLKaaS	nytDPlLAFV	tnYtYSLGqD
A. pediades	NIIqRHGARF	PTSGaGtRiq	AaVKKLQsak	TytDPRLDFL	tnYtYTLGhD
P. lycii	NLIqRHGARW	PTSGarsRqv	AaVAKIQmar	PftDPKYEFL	NdFvYkFGvA
A. terreus 9a1	QVLARHGARs	PThSKTKaYA	AtIAaIQKSA	TaFpGKYAFL	QSYNYSLDSE
A. terreus cbs	QVLARHGARs	PTdSKTKaYA	AtIAaIQKNA	TaLpGKYAFL	KSYNYSMGSE
A. niger var. *awamori*	QVLSRHGARY	PTeSKGKKYS	ALIEeIQQNv	TtFDGKYAFL	KTYNYSLGAD
A. niger T213	QVLSRHGARY	PTeSKGKKYS	ALIEeIQQNv	TtFDGKYAFL	KTYNYSLGAD
A. niger NRRL3135	QVLSRHGARY	PTdSKGKKYS	ALIEeIQQNA	TtFDGKYAFL	KTYNYSLGAD
A. fumigatus ATCC13073	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus ATCC32722	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus ATCC58128	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus ATCC26906	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKFAFL	KTYNYTLGAD
A. fumigatus ATCC32239	QVLSRHGARY	PTASKSKKYk	kLVtaIQKNA	TeFKGKFAFL	ETYNYTLGAD
E. nidulans	QVLSRHGARY	PTeSKSKaYS	GLIEaIQKNA	TsFwGQYAFL	ESYNYTLGAD
T. thermophilus	QLLSRHGARY	PTSSKTElYS	qLIsRIQKtA	TaYKGyYAFL	KdYrYqLGAN
T. lanuginosus	QVLSRHGARY	PTAhKSEvYA	ELLQRIQDtA	TeFKGDFAFL	RdYaYhLGAD
M. thermophila	QVLSRHGARa	PTlkRAasYv	DLIDRIHhGA	isYgPgYEFL	RTYDYTLGAD
Consensus Seq. 11	**QVLSRHGARY**	**PTSSKSKKYS**	**ALIERIQKNA**	**T-FKGKYAFL**	**KTYNYTLGAD**

Fig. 6a

	101				150
P. involutus (phyA1)	DLvPFGAaQs	fDAGqEaFaR	YskLvSKNnL	PFIRAdGSDR	VVDSAtNWtA
P. involutus (phyA2)	DLvPFGAaQs	fDAGLEvFaR	YskLvSsDnL	PFIRSdGSDR	VVDTAtNWtA
T. pubescens	sLveLGAtQs	sEAGqEaFtR	YsSLvSaDeL	PFVRASGSDR·	VVATANNWtA
A. pediades	DLvPFGAlQs	sQAGeEtFQR	YsfLvSKEnL	PFVRASSSNR	VVDSAtNWtE
P. lycii	DLlPFGANQs	hQTGtDMYtR	YsTLfEgGdV	PFVRAAGdQR	VVDSStNWtA
A. terreus 9a1	ELTPFGrNQL	rDlGaQFYeR	YNAL.TRHIn	PFVRATDAsR	VhESAEKFVE
A. terreus cbs	NLTPFGrNQL	qDlGaQFYRR	YDTL.TRHIn	PFVRAADSsR	VhESAEKFVE
A. niger var. awamori	DLTPFGEQEL	VNSGIKFYQR	YESL.TRNII	PFIRSSGSsR	VIASGEKFIE
A. niger T213	DLTPFGEQEL	VNSGIKFYQR	YESL.TRNII	PFIRSSGSsR	VIASGEKFIE
A. niger NRRL3135	DLTPFGEQEL	VNSGIKFYQR	YESL.TRNIV	PFIRSSGSsR	VIASGKKFIE
A. fumigatus ATCC13073	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARSVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus ATCC32722	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARSVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus ATCC58128	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARSVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus ATCC26906	DLTAFGEQQL	VNSGIKFYQR	YKAL.ARSVV	PFIRASGSDR	VIASGEKFIE
A. fumigatus ATCC32239	DLTPFGEQQM	VNSGIKFYQK	YKAL.AgSVV	PFIRSSGSDR	VIASGEKFIE
E. nidulans	DLTiFGENQM	VDSGaKFYRR	YKnL.ARKnt	PFIRASGSDR	VVASAEKFIN
T. thermophilus	DLTPFGENQM	IQlGIKFYnH	YKSL.ARNaV	PFVRCSGSDR	VIASGrlFIE
T. lanuginosus	NLTRFGEEQM	MESGrQFYHR	YREq.AREIV	PFVRAAGSAR	VIASAEfFnr
M. thermophila	ELTRtGQQQM	VNSGIKFYRR	YRAL.ARKsI	PFVRTAGqDR	VVhSAENFtQ
Consensus Seq. 11	**DLTPFGENQM**	**VNSGIKFYRR**	**YKAL-ARNIV**	**PFVRASGSDR**	**VIASAEKFIE**

	151				200
P. involutus (phyA1)	GFaSA.....	..shNtvqPk	LNLILPQ..T	gNDTLEDNMC	PAaGD.....
P. involutus (phyA2)	GFaSA.....	..srNaiqPk	LDLILPQ..T	gNDTLEDNMC	PAaGE.....
T. pubescens	GFalA.....	..ssNsiTPV	LSVIISE..A	gNDTLDDNMC	PAaGD.....
A. pediades	GFsAA.....	..shHvlNPI	LfVILSE..S	LNDTLDDAMC	PnaGs.....
P. lycii	GFgdA.....	..sgEtvlPt	LQVVLQE..E	gNcTLcNNMC	PnevD.....
A. terreus 9a1	GFQTARqDDh	hAnpHQPSPr	VDVaIPEGSA	YNNTLEHSLC	TAFEs...ST
A. terreus cbs	GFQNARqGDP	hAnpHQPSPr	VDVVIPEGTA	YNNTLEHSIC	TAFEA...ST
A. niger var. awamori	GFQSTKLkDP	rAqpgQSSPk	IDVVISEASS	sNNTLDpGtC	TvFED...Se
A. niger T213	GFQSTKLkDP	rAqpgQSSPk	IDVVISEASS	sNNTLDpGtC	TvFED...Se
A. niger NRRL3135	GFQSTKLkDP	rAqpgQSSPk	IDVVISEASS	sNNTLDpGtC	TvFED...Se
A. fumigatus ATCC13073	GFQqAKLADP	gAt.NRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEA...Sq
A. fumigatus ATCC32722	GFQqAKLADP	gAt.NRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEA...Sq
A. fumigatus ATCC58128	GFQqAKLADP	gAt.NRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEA...Sq
A. fumigatus ATCC26906	GFQqAKLADP	gAt.NRAAPa	ISVIIPESeT	FNNTLDHGVC	TkFEA...Sq
A. fumigatus ATCC32239	GFQqANVADP	gAt.NRAAPV	ISVIIPESeT	YNNTLDHSVC	TnFEA...Se
E. nidulans	GFRkAQLhDh	g.s.gQATPV	VNVIIPEidG	FNNTLDHStC	vSFEN...de
T. thermophilus	GFQSAKVlDP	hSdkHDAPPt	INVIIeEGPS	YNNTLDtGsC	PvFED...SS
T. lanuginosus	GFQdAKdrDP	rSnkDQAePV	INVIISEETG	sNNTLDgltC	PAaEE...AP
M. thermophila	GFHSAlLADR	gStvRPTlPy	dmVVIPETAG	aNNTLHNDLC	TAFEEgpyST
Consensus Seq. 11	**GFQSAKLADP**	**-A--HQASPV**	**INVIIPEGSG**	**YNNTLDHGLC**	**TAFED---ST**

Fig. 6b

	201 250
P. involutus (phyA1)	.SDpqvnaWl AVafPSItAR LNAaaPSVNL TDtDafNLVs LCAFlTVSK.
P. involutus (phyA2)	.SDpqvDaWl AsafPSVtAQ LNAaaPGaNL TDADafNLVs LCPFmTVSK.
T. pubescens	.SDpqvnQWl AqFAPPMtAR LNAgaPGaNL TDtDtyNLLt LCPFETVAt.
A. pediades	.SDpqtGiWT SIYGTPIanR LNqqaPGaNI TAADVsNLIp LCAFETIvK.
P. lycii	.GDESt.tWl GVFAPnItAR LNAaaPSaNL SDsDaLtLMD MCPFDTLSs.
A. terreus 9a1	VGDDAvANFT AVFAPAIaqR LEAdLPGVQL StDDVVNLMA MCPFETVSlT
A. terreus cbs	VGDAAADNFT AVFAPAIakR LEAdLPGVQL SADDVVNLMA MCPFETVSlT
A. niger var. awamori	LADtvEANFT AtFAPSIRqR LEndLSGVtL TDtEVtyLMD MCSFDTIStS
A. niger T213	LADtvEANFT AtFAPSIRqR LEndLSGVtL TDtEVtyLMD MCSFDTIStS
A. niger NRRL3135	LADtvEANFT AtFvPSIRqR LEndLSGVtL TDtEVtyLMD MCSFDTIStS
A. fumigatus ATCC13073	LGDEvAANFT ALFAPdIRAR aEkhLPGVtL TDEDVVSLMD MCSFDTVART
A. fumigatus ATCC32722	LGDEvAANFT ALFAPdIRAR aEkhLPGVtL TDEDVVSLMD MCSFDTVART
A. fumigatus ATCC58128	LGDEvAANFT ALFAPdIRAR aEkhLPGVtL TDEDVVSLMD MCSFDTVART
A. fumigatus ATCC26906	LGDEvAANFT ALFAPdIRAR aKkhLPGVtL TDEDVVSLMD MCSFDTVART
A. fumigatus ATCC32239	LGDEvEANFT ALFAPAIRAR IEkhLPGVQL TDDDVVSLMD MCSFDTVART
E. nidulans	rADEiEANFT AIMGPPIRkR LEndLPGIKL TNENVIyLMD MCSFDTMART
T. thermophilus	gGHDAQEKFA kqFAPAIlEK IKDhLPGVDL AvsDVpyLMD LCPFETLARn
T. lanuginosus	.DptqpAEFl qVFGPRVlkK ItkhMPGVNL TlEDVplFMD LCPFDTVGsd
M. thermophila	IGDDAQDtYl StFAGPItAR VNAnLPGaNL TDADtVaLMD LCPFETVAsS
Consensus Seq. 11	**LGDDAEANFT AVFAPPIRAR LEA-LPGVNL TDEDVVNLMD MCPFDTVART**

	251 300
P. involutus (phyA1)	....ekkSdF CtLFegiPGs FeaFAYggdL dKFYGtGyGQ
P. involutus (phyA2)	....eqkSdF CtLFegiPGs FeaFAYagdL dKFYGtGyGQ
T. pubescens	....errSeF CDIYeelqAE .daFAYnadL dKFYGtGyGQ
A. pediades	....etpSPF CNLF..TPEE FaQFEYFgdL dKFYGtGyGQ
P. lycii	....gnaSPF CDLF..TAEE YvsYEYYydL dKYYGtGPGN
A. terreus 9a1	dD..Aht... ......LSPF CDLF..TAtE WtQYNYLlSL dKYYGYGGGN
A. terreus cbs	dD..Aht... ......LSPF CDLF..TAAE WtQYNYLlSL dKYYGYGGGN
A. niger var. awamori	Tv..DTK... ......LSPF CDLF..ThDE WiHYDYLQSL kKYYGHGAGN
A. niger T213	Tv..DTK... ......LSPF CDLF..ThDE WiHYDYLRSL kKYYGHGAGN
A. niger NRRL3135	Tv..DTK... ......LSPF CDLF..ThDE WiNYDYLQSL kKYYGHGAGN
A. fumigatus ATCC13073	SD..ASQ... ......LSPF CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
A. fumigatus ATCC32722	SD..ASQ... ......LSPF CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
A. fumigatus ATCC58128	SD..ASQ... ......LSPF CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
A. fumigatus ATCC26906	SD..ASQ... ......LSPF CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
A. fumigatus ATCC32239	AD..ASE... ......LSPF CAIF..ThNE WkKYDYLQSL gKYYGYGAGN
E. nidulans	AH..GTE... ......LSPF CAIF..TEKE WlQYDYLQSL sKYYGYGAGS
T. thermophilus	ht..DT.... ......LSPF CALs..TqEE WqaYDYYQSL gKYYGnGGGN
T. lanuginosus	PvlfPrQ... ......LSPF CHLF..TADD WmaYDYYyTL dKYYSHGGGS
M. thermophila	SsdpATadag ggngrpLSPF CrLF..SEsE WraYDYLQSV gKWYGYGPGN
Consensus Seq. 11	**SD--ATQ--- ------LSPF CDLF--TADE W-QYDYLQSL -KYYGYGAGN**

Fig. 6c

	301 350
P. involutus (phyA1)	eLGPvQGVGY vNELIARLTN S.AVRDNTqT NRTLDASPvT FPLNkTFYAD
P. involutus (phyA2)	ALGPvQGVGY iNELLARLTN S.AVNDNTqT NRTLDAaPDT FPLNkTMYAD
T. pubescens	PLGPvQGVGY iNELIARLTa q.nVsDHTqT NsTLDSSPET FPLNrTLYAD
A. pediades	PLGPvQGVGY iNELLARLTE m.PVRDNTqT NRTLDSSPlT FPLDrSIYAD
P. lycii	ALGPvQGVGY vNELLARLTg q.AVRDETqT NRTLDSDPAT FPLNrTFYAD
A. terreus 9a1	PLGPvQGVGW aNELMARLTR A.PVHDHTCv NNTLDASPAT FPLNATLYAD
A. terreus cbs	PLGPvQGVGW aNELIARLTR S.PVHDHTCv NNTLDANPAT FPLNATLYAD
A. niger var. *awamori*	PLGPTQGVGY aNELIARLTH S.PVHDDTSS NHTLDSNPAT FPLNSTLYAD
A. niger T213	PLGPTQGVGY aNELIARLTH S.PVHDDTSS NHTLDSNPAT FPLNSTLYAD
A. niger NRRL3135	PLGPTQGVGY aNELIARLTH S.PVHDDTSS NHTLDSSPAT FPLNSTLYAD
A. fumigatus ATCC13073	PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTLvSNPAT FPLNATMYvD
A. fumigatus ATCC32722	PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTLvSNPAT FPLNATMYvD
A. fumigatus ATCC58128	PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTLvSNPAT FPLNATMYvD
A. fumigatus ATCC26906	PLGPAQGIGF tNELIARLTR S.PVQDHTST NsTLvSNPAT FPLNATMYvD
A. fumigatus ATCC32239	PLGPAQGIGF tNELIARLTN S.PVQDHTST NsTLDSDPAT FPLNATIYvD
E. nidulans	PLGPAQGIGF tNELIARLTQ S.PVQDNTST NHTLDSNPAT FPLDrkLYAD
T. thermophilus	PLGPAQGVGF vNELIARMTH S.PVQDYTTv NHTLDSNPAT FPLNATLYAD
T. lanuginosus	AFGPSRGVGF vNELIARMTg NlPVKDHTTv NHTLDdNPET FPLDAvLYAD
M. thermophila	PLGPTQGVGF vNELLARLA. GvPVRDgTST NRTLDGDPrT FPLGrPLYAD
Consensus Seq. 11	**PLGPAQGVGF -NELIARLTH S-PVQDHTST NHTLDSNPAT FPLNATLYAD**

	351 400
P. involutus (phyA1)	FSHDNlMVAV FsAMGLFrqP aPLSTSvpNP wrt.....Wr TSSlVPFSGR
P. involutus (phyA2)	FSHDNlMVAV FsAMGLFrqS aPLSTSTpDP nrt.....Wl TSSvVPFSAR
T. pubescens	FSHDNqMVAI FsAMGLFNqS aPLdPTTpDP art.....Fl vkkiVPFSAR
A. pediades	LSHDNqMIAI FsAMGLFNqS sPLdPSfpNP krt.....Wv TSRltPFSAR
P. lycii	FSHDNTMVPI FaALGLFNAT a.LdPlkpDe nrl.....Wv DSklVPFSGH
A. terreus 9a1	FSHDSnLVSI FWALGLYNGT aPLSqTSVES Vs..QTDGYA AAWTVPFAAR
A. terreus cbs	FSHDSnLVSI FWALGLYNGT KPLSqTTVEd It..rTDGYA AAWTVPFAAR
A. niger var. *awamori*	FSHDNGIISI LFALGLYNGT KPLSTTTVEN It..QTDGFS SAWTVPFASR
A. niger T213	FSHDNGIISI LFALGLYNGT KPLSTTTVEN It..QTDGFS SAWTVPFASR
A. niger NRRL3135	FSHDNGIISI LFALGLYNGT KPLSTTTVEN It..QTDGFS SAWTVPFASR
A. fumigatus ATCC13073	FSHDNSMVSI FFALGLYNGT EPLSrTSVES ak..ElDGYS ASWvVPFGAR
A. fumigatus ATCC32722	FSHDNSMVSI FFALGLYNGT gPLSrTSVES ak..ElDGYS ASWvVPFGAR
A. fumigatus ATCC58128	FSHDNSMVSI FFALGLYNGT EPLSrTSVES ak..ElDGYS ASWvVPFGAR
A. fumigatus ATCC26906	FSHDNSMVSI FFALGLYNGT EPLSrTSVES ak..ElDGYS ASWvVPFGAR
A. fumigatus ATCC32239	FSHDNGMIPI FFAMGLYNGT EPLSqTSeES tk..ESNGYS ASWAVPFGAR
E. nidulans	FSHDNSMISI FFAMGLYNGT QPLSmdSVES Iq..EmDGYA ASWTVPFGAR
T. thermophilus	FSHDNTMtSI FaALGLYNGT akLSTTeIKS Ie..ETDGYS AAWTVPFGGR
T. lanuginosus	FSHDNTMtGI FsAMGLYNGT KPLSTSkIQP ptgaAADGYA ASWTVPFAAR
M. thermophila	FSHDNdMMGV LgALGaYDGv pPLdkTArrd ..peElGGYA ASWAVPFAAR
Consensus Seq. 11	**FSHDNTMVSI FFALGLYNGT KPLSTTSVES I---ETDGYA ASWTVPFAAR**

Fig. 6d

	401				450
P. involutus (*phyA1*)	mvVErLsC..	fGt.......	........Tk	VRVLVQDQVq	PLEfCGgDRn
P. involutus (*phyA2*)	maVErLsC..	AGt.......	........Tk	VRVLVQDQVq	PLEfCGgDQd
T. pubescens	mvVErLDC..	GGa.......	........Qs	VRLLVNDaVq	PLafCGaDts
A. pediades	mvtErLlCQr	DGtGsGGpsr	imrNgnvQTF	VRILVNDaLq	PLkfCGgDmd
P. lycii	mtVEkLaC..	....	.....sgKea	VRVLVNDaVq	PLEfCGg.vd
A. terreus 9a1	AYVEMMQCrA	....	..EK...EPL	VRVLVNDRVM	PLHGCPtDKL
A. terreus cbs	AYIEMMQCrA	....	..EK...QPL	VRVLVNDRVM	PLHGCAVDNL
A. niger var. *awamori*	lYVEMMQCQA	....	..EQ...EPL	VRVLVNDRVV	PLHGCPIDaL
A. niger T213	lYVEMMQCQA	....	..EQ...EPL	VRVLVNDRVV	PLHGCPIDaL
A. niger NRRL3135	lYVEMMQCQA	....	..EQ...EPL	VRVLVNDRVV	PLHGCPVDaL
A. fumigatus ATCC13073	AYfEtMQCKS	....	..EK...EPL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus ATCC32722	AYfEtMQCKS	....	..EK...EPL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus ATCC58128	AYfEtMQCKS	....	..EK...ESL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus ATCC26906	AYfEtMQCKS	....	..EK...EPL	VRaLINDRVV	PLHGCDVDKL
A. fumigatus ATCC32239	AYfEtMQCKS	....	..EK...EPL	VRaLINDRVV	PLHGCAVDKL
E. nidulans	AYfELMQCE.	....	..KK...EPL	VRVLVNDRVV	PLHGCAVDKF
T. thermophilus	AYIEMMQCDD	....	..sD...EPV	VRVLVNDRVV	PLHGCEVDsL
T. lanuginosus	AYVELLRCET	ETsSeEEeEG	..ED...EPF	VRVLVNDRVV	PLHGCrVDRW
M. thermophila	iYVEkMRCsG	GGgGgGGgEG	..rQekdEeM	VRVLVNDRVM	TLkGCGaDEr
Consensus Seq. 11	**AYVEMMQCEA**	**GG-G-GG-EG**	**--EK---EPL**	**VRVLVNDRVV**	**PLHGCGVDKL**

	451			482
P. involutus (*phyA1*)	GlCtLAKFVE	SqTFARSDga	GDFEKCFAts	a~
P. involutus (*phyA2*)	GlCaLDKFVE	SqAYARSGga	GDFEKCLAtt	v~
T. pubescens	GvCtLDAFVE	SqAYARNDge	GDFEKCFAt~	~~
A. pediades	SlCtLEAFVE	SqkYAReDgq	GDFEKCFD~~	~~
P. lycii	GvCELsAFVE	SqTYAReNgq	GDFAKCgfvp	se
A. terreus 9a1	GRCKrDAFVA	GLSFAQAG..	GNWADCF~~~	~~
A. terreus cbs	GRCKrDDFVE	GLSFARAG..	GNWAECF~~~	~~
A. niger var. *awamori*	GRCtrDsFVr	GLSFARSG..	GDWAECsA~~	~~
A. niger T213	GRCtrDsFVr	GLSFARSG..	GDWAECFA~~	~~
A. niger NRRL3135	GRCtrDsFVr	GLSFARSG..	GDWAECFA~~	~~
A. fumigatus ATCC13073	GRCKLNDFVK	GLSWARSG..	GNWGECFS~~	~~
A. fumigatus ATCC32722	GRCKLNDFVK	GLSWARSG..	GNWGECFS~~	~~
A. fumigatus ATCC58128	GRCKLNDFVK	GLSWARSG..	GNWGECFS~~	~~
A. fumigatus ATCC26906	GRCKLNDFVK	GLSWARSG..	GNWGECFS~~	~~
A. fumigatus ATCC32239	GRCKLKDFVK	GLSWARSG..	GNSEQSFS~~	~~
E. nidulans	GRCtLDDWVE	GLNFARSG..	GNWktCFTl~	~~
T. thermophilus	GRCKrDDFVr	GLSFARqG..	GNWEGCYAas	e~
T. lanuginosus	GRCRrDEWIK	GLTFARqG..	GHWDrCF~~~	~~
M. thermophila	GmCtLErFIE	SMAFARGN..	GKWDlCFA~~	~~
Consensus Seq. 11	**GRCKLDDFVE**	**GLSFARSG--**	**GNWAECFA--**	**--**

Fig. 6e

```
     M  G  V  F  V  V  L  L  S  I  A  T  L  F  G  S  T  S  G  T       20
     ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC
  1  ---------+---------+---------+---------+---------+---------+   60
     TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGTGTAGGCCATGG

     A  L  G  P  R  G  N  S  H  S  C  D  T  V  D  G  G  Y  Q  C       40
     GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
 61  ---------+---------+---------+---------+---------+---------+   120
     CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

     F  P  E  I  S  H  L  W  G  T  Y  S  P  Y  F  S  L  A  D  E       60
     TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA
121  ---------+---------+---------+---------+---------+---------+   180
     AAGGGTCTTTAAAGAGTGAACACCCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT

     S  A  I  S  P  D  V  P  D  D  C  R  V  T  F  V  Q  V  L  S       80
     TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT
187  ---------+---------+---------+---------+---------+---------+   240
     AGACGATAAAGAGGTCTGCAAGGTCTGCTGACATCTCAATGAAAGCAAGTTCAAAACAGA

     R  H  G  A  R  Y  P  T  S  S  A  S  K  A  Y  S  A  L  I  E      100
     AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA
241  ---------+---------+---------+---------+---------+---------+   300
     TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGAATGAGACGAAACTAACTT

     A  I  Q  K  N  A  T  A  F  K  G  K  Y  A  F  L  K  T  Y  N      120
     GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
301  ---------+---------+---------+---------+---------+---------+   360
     CGATAAGTTTTCTTGCGATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTG

     Y  T  L  G  A  D  D  L  T  P  F  G  E  N  Q  M  V  N  S  G      140
     TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT
361  ---------+---------+---------+---------+---------+---------+   420
     ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTTGGTTTACCAATTGAGACCA

     I  K  F  Y  R  R  Y  K  A  L  A  R  K  I  V  P  F  I  R  A      160
     ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT
421  ---------+---------+---------+---------+---------+---------+   480
     TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

     S  G  S  D  R  V  I  A  S  A  E  K  F  I  E  G  F  Q  S  A      180
     TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481  ---------+---------+---------+---------+---------+---------+   540
     AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAAAGGTTAGACGA

     K  L  A  D  P  G  S  Q  P  H  Q  A  S  P  V  I  N  V  I  I      200
     AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT
541  ---------+---------+---------+---------+---------+---------+   600
     TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTCGAAGAGGTCAATAATTGCACTAGTAA

     P  E  G  S  G  Y  N  N  T  L  D  H  G  T  C  T  A  F  E  D      220
     CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC
601  ---------+---------+---------+---------+---------+---------+   660
     GGTCTTCCTAGGCCAATGTTGTTGTGAAACCTGGTGCCATGAACATGACGAAAGCTTCTG
```

Fig. 7a

```
      S  E  L  G  D  D  V  E  A  N  F  T  A  L  F  A  P  A  I  R    240
      TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA
 661  ---------+---------+---------+---------+---------+---------+  720
      AGACTTAATCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAGGTCGATAATCT

      A  R  L  E  A  D  L  P  G  V  T  L  T  D  E  D  V  V  Y  L    260
      GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG
 721  ---------+---------+---------+---------+---------+---------+  780
      CGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGCTTCTGCAACAAATGAAC

      M  D  M  C  P  F  D  T  V  A  R  T  S  D  A  T  E  L  S  P    280
      ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA
 781  ---------+---------+---------+---------+---------+---------+  840
      TACCTGTACACAGGTAAGCTGTGACAGCGATCTTGAAGACTGCGATGACTTAACAGAGGT

      F  C  A  L  F  T  H  D  E  W  I  Q  Y  D  Y  L  Q  S  L  G    300
      TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT
 841  ---------+---------+---------+---------+---------+---------+  900
      AAGACACGAAACAAGTGAGTGCTGCTTACCTAGGTTATGCTGATGAACGTTTCGAACCCA

      K  Y  Y  G  Y  G  A  G  N  P  L  G  P  A  Q  G  V  G  F  A    320
      AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT
 901  ---------+---------+---------+---------+---------+---------+  960
      TTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTCGAGTTCCACAACCAAAGCGA

      N  E  L  I  A  R  L  T  H  S  P  V  Q  D  H  T  S  T  N  H    340
      AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
 961  ---------+---------+---------+---------+---------+---------+ 1020
      TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

      T  L  D  S  N  P  A  T  F  P  L  N  A  T  L  Y  A  D  F  S    360
      ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
1021  ---------+---------+---------+---------+---------+---------+ 1080
      TGAAACCTGAGATTGGGTCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

      H  D  N  T  M  I  S  I  F  F  A  L  G  L  Y  N  G  T  K  P    380
      CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA
1081  ---------+---------+---------+---------+---------+---------+ 1140
      GTGCTGTTGTGATACTATAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGGTTCGGT

      L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  S  A  S  W  T    400
      TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT
1141  ---------+---------+---------+---------+---------+---------+ 1200
      AACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

      V  P  F  A  A  R  A  Y  V  E  M  M  Q  C  Q  A  E  K  E  P    420
      GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA
1201  ---------+---------+---------+---------+---------+---------+ 1260
      CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACAGTTCGACTTTTCCTTGGT

      L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  A  V  D  K    440
      TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261  ---------+---------+---------+---------+---------+---------+ 1320
      AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACTGTTC
```

Fig. 7b

```
       L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G    460
       TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
  1321 ---------+---------+---------+---------+---------+---------+ 1380
       AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

       N  W  A  E  C  F  A  *    467
       AACTGGGCTGAATGTTTCGCTTAA
  1381 ---------+---------+---- 1410
       TTGACCCGACTTACAAAGCGAATT
```


Fig. 7c

```
      M  G  V  F  V  V  L  L  S  I  A  T  L  F  G  S  T  S  G  T     20
      ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC
   1  ---------+---------+---------+---------+---------+---------+  60
      TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGTGTAGGCCATGG

      A  L  G  P  R  G  N  S  H  S  C  D  T  V  D  G  G  Y  Q  C     40
      GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
  61  ---------+---------+---------+---------+---------+---------+  120
      CGGAACCCAGGAGCACCATTGAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

      F  P  E  I  S  H  L  W  G  T  Y  S  P  F  F  S  L  A  D  E     60
      TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA
 121  ---------+---------+---------+---------+---------+---------+  180
      AAGGGTCTTTAAAGAGTGAACACCCCATGTATGAGAGGTAAGAAGAGAAACCGACTGCTT

      S  A  I  S  P  D  V  P  K  G  C  R  V  T  F  V  Q  V  L  S     80
      TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT
 181  ---------+---------+---------+---------+---------+---------+  240
      AGACGATAAAGAGGTCTGCAAGGTTTCCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

      R  H  G  A  R  Y  P  T  S  S  A  S  K  A  Y  S  A  L  I  E     100
      AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA
 241  ---------+---------+---------+---------+---------+---------+  300
      TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGCATGAGACGAAACTAACTT

      A  I  Q  K  N  A  T  A  F  K  G  K  Y  A  F  L  K  T  Y  N     120
      GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
 301  ---------+---------+---------+---------+---------+---------+  360
      CGATAAGTTTTCTTGCGATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTG

      Y  T  L  G  A  D  D  L  T  P  F  G  E  Q  Q  M  V  N  S  G     140
      TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT
 361  ---------+---------+---------+---------+---------+---------+  420
      ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTGTTGTTTACCAATTGAGACCA

      I  K  F  Y  R  R  Y  K  A  L  A  R  K  I  V  P  F  I  R  A     160
      ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT
 421  ---------+---------+---------+---------+---------+---------+  480
      TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

      S  G  S  D  R  V  I  A  S  A  E  K  F  I  E  G  F  Q  S  A     180
      TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT
 481  ---------+---------+---------+---------+---------+---------+  540
      AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAAAGGTTAGACGA

      K  L  A  D  P  G  A  N  P  H  Q  A  S  P  V  I  N  V  I  I     200
      AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT
 541  ---------+---------+---------+---------+---------+---------+  600
      TTCAACCGACTGGGTCCACGATTGGGTGTGGTTCGAAGAGGTCAATAATTGCAATAATAA

      P  E  G  A  G  Y  N  N  T  L  D  H  G  L  C  T  A  F  E  E     220
      CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA
 601  ---------+---------+---------+---------+---------+---------+  660
      GGTCTTCCACGACCAATGTTGTTGTGAAACCTGGTGCCAAACACATGACGAAAGCTTCTT
```

Fig. 8a

```
         S  E  L  G  D  D  V  E  A  N  F  T  A  V  F  A  P  P  I  R    240
         TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA
    661  ---------+---------+---------+---------+---------+---------+  720
         AGACTTAACCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAGGTGGTTAATCT

         A  R  L  E  A  H  L  P  G  V  N  L  T  D  E  D  V  V  N  L    260
         GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG
    721  ---------+---------+---------+---------+---------+---------+  780
         CGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGCAACAATTGAAC

         M  D  M  C  P  F  D  T  V  A  R  T  S  D  A  T  Q  L  S  P    280
         ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA
    781  ---------+---------+---------+---------+---------+---------+  840
         TACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAGTTAACAGAGGT

         F  C  D  L  F  T  H  D  E  W  I  Q  Y  D  Y  L  Q  S  L  G    300
         TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT
    841  ---------+---------+---------+---------+---------+---------+  900
         AAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACGTTAGAAACCCA

         K  Y  Y  G  Y  G  A  G  N  P  L  G  P  A  Q  G  V  G  F  V    320
         AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT
    901  ---------+---------+---------+---------+---------+---------+  960
         TTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTCGAGTTCCACAACCAAAGCAA

         N  E  L  I  A  R  L  T  H  S  P  V  Q  D  H  T  S  T  N  H    340
         AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
    961  ---------+---------+---------+---------+---------+---------+ 1020
         TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

         T  L  D  S  N  P  A  T  F  P  L  N  A  T  L  Y  A  D  F  S    360
         ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
   1021  ---------+---------+---------+---------+---------+---------+ 1080
         TGAAACCTGAGATTGGGTCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

         H  D  N  T  M  V  S  I  F  F  A  L  G  L  Y  N  G  T  K  P    380
         CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA
   1081  ---------+---------+---------+---------+---------+---------+ 1140
         GTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGATTCGGT

         L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  S  A  S  W  T    400
         TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT
   1141  ---------+---------+---------+---------+---------+---------+ 1200
         AACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

         V  P  F  A  A  R  A  Y  V  E  M  M  Q  C  E  A  E  K  E  P    420
         GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
   1201  ---------+---------+---------+---------+---------+---------+ 1260
         CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACACTTCGACTTTTCCTTGGT

         L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  G  V  D  K    440
         TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG
   1261  ---------+---------+---------+---------+---------+---------+ 1320
         AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACCACAACTGTTC
```

Fig. 8b

```
      L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G    460
      TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321  ---------+---------+---------+---------+---------+---------+ 1380
      AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

      N  W  E  E  C  F  A  *    467
      AACTGGGAAGAATGTTTCGCTTAA
1381  ---------+---------+---- 1404
      TTGACCCTTCTTACAAAGCGAATT
```


Fig. 8c

```
     M  G  V  F  V  V  L  L  S  I  A  T  L  F  G  S  T  S  G  T    20
     ATGGGGGTTTTCGTCGTTCTATTATCTATCGCGACTCTGTTCGGCAGCACATCGGGCACT
1    ---------+---------+---------+---------+---------+---------+  60
     TACCCCCAAAAGCAGCAAGATAATAGATAGCGCTGAGACAAGCCGTCGTGTAGCCCGTGA

     A  L  G  P  R  G  N  H  S  K  S  C  D  T  V  D  L  G  Y  Q    40
     GCGCTGGGCCCCCGTGGAAATCACTCCAAGTCCTGCGATACGGTAGACCTAGGGTACCAG
61   ---------+---------+---------+---------+---------+---------+  120
     CGCGACCCGGGGGCACCTTTAGTGAGGTTCAGGACGCTATGCCATCTGGATCCCATGGTC

     C  S  P  A  T  S  H  L  W  G  T  Y  S  P  Y  F  S  L  E  D    60
     TGCTCCCCTGCGACTTCTCATCTATGGGGCACGTACTCGCCATaCTTTTCGCTCGAGGAC
121  ---------+---------+---------+---------+---------+---------+  180
     ACGAGGGGACGCTGAAGAGTAGATACCCCGtgCATGAGCGGTAtGAAAAGCGAGCTCCTG

     E  L  S  V  S  S  K  L  P  K  D  C  R  I  T  L  V  Q  V  L    80
     GAGCTGTCCGTGTCGAGTAAGCTTCCCAAGGATTGCCGGATCACCTTGGTACAGGTGCTA
181  ---------+---------+---------+---------+---------+---------+  240
     CTCGACAGGCACAGCTCATTCGAAGGGTTCCTAACGGCCTAGTGGAACCATGTCCACGAT

     S  R  H  G  A  R  Y  P  T  S  S  K  S  K  K  Y  K  K  L  I    100
     TCGCGCCATGGAGCGCGGTACCCAACCAGCTCCAAGAGCAAAAAGTATAAGAAGCTTaTt
241  ---------+---------+---------+---------+---------+---------+  300
     AGCGCGGTACCTCGCGCCATGGGTTGGTCGAGGTTCTCGTTTTTCATATTCTTCGAAtAa

     T  A  I  Q  A  N  A  T  D  F  K  G  K  Y  A  F  L  K  T  Y    120
     ACGGCGATCCAGGCCAATGCCACCGACTTCAAGGGCAAGTacGCCTTTTTGAAGACGTAC
301  ---------+---------+---------+---------+---------+---------+  360
     TGCCGCTAGGTCCGGTTACGGTGGCTGAAGTTCCCGTTCAtgCGGAAAAACTTCTGCATG

     N  Y  T  L  G  A  D  D  L  T  P  F  G  E  Q  Q  L  V  N  S    140
     AACTATACTCTGGGTGCGGATGACCTCACTCCCTTTGGGGAGCAGCAGCTGGTGAACTCG
361  ---------+---------+---------+---------+---------+---------+  420
     TTGATATGAGACCCACGCCTACTGGAGTGAGGGAAACCCCTCGTCGTCGACCACTTGAGC

     G  I  K  F  Y  Q  R  Y  K  A  L  A  R  S  V  V  P  F  I  R    160
     GGCATCAAGTTCTACCAGAGGTACAAGGCTCTGGCGCGCAGTGTGGTGCCGTTTATTCGC
421  ---------+---------+---------+---------+---------+---------+  480
     CCGTAGTTCAAGATGGTCTCCATGTTCCGAGACCGCGCGTCACACCACGGCAAATAAGCG

     A  S  G  S  D  R  V  I  A  S  G  E  K  F  I  E  G  F  Q  Q    180
     GCCTCAGGCTCGGACCGGGTTATTGCTTCGGGAGAGAAGTTCATCGAGGGGTTCCAGCAG
481  ---------+---------+---------+---------+---------+---------+  540
     CGGAGTCCGAGCCTGGCCCAATAACGAAGCCCTCTCTTCAAGTAGCTCCCCAAGGTCGTC

     A  K  L  A  D  P  G  A  T  N  R  A  A  P  A  I  S  V  I  I    200
     GCGAAGCTGGCTGATCCTGGCGCGACGAACCGCGCCGCTCCGGCGATTAGTGTGATTATT
541  ---------+---------+---------+---------+---------+---------+  600
     CGCTTCGACCGACTAGGACCGCGCTGCTTGGCGCGGCGAGGCCGCTAATCACACTAATAA

     P  E  S  E  T  F  N  N  T  L  D  H  G  V  C  T  K  F  E  A    220
     CCGGAGAGCGAGACGTTCAACAATACGCTGGACCACGGTGTGTGCACGAAGTTTGAGGCG
601  ---------+---------+---------+---------+---------+---------+  660
     GGCCTCTCGCTCTGCAAGTTGTTATGCGACCTGGTGCCACACACGTGCTTCAAACTCCGC
```

Fig. 9a

```
     S  Q  L  G  D  E  V  A  A  N  F  T  A  L  F  A  P  D  I  R       240
     AGTCAGCTGGGAGATGAGGTTGCGGCCAATTTCACTGCGCTCTTTGCACCCGACATCCGA
661  ---------+---------+---------+---------+---------+---------+ 720
     TCAGTCGACCCTCTACTCCAACGCCGGTTAAAGTGACGCGAGAAACGTGGGCTGTAGGCT

     A  R  L  E  K  H  L  P  G  V  T  L  T  D  E  D  V  V  S  L       260
     GCTCGCCtCGAGAAGCATCTTCCTGGCGTGACGCTGACAGACGAGGACGTTGTCAGTCTA
721  ---------+---------+---------+---------+---------+---------+ 780
     CGAGCGGaGCTCTTCGTAGAAGGACCGCACTGCGACTGTCTGCTCCTGCAACAGTCAGAT

     M  D  M  C  P  F  D  T  V  A  R  T  S  D  A  S  Q  L  S  P       280
     ATGGACATGTGTcCGTTTGATACGGTAGCGCGCACCAGCGACGCAAGTCAGCTGTCACCG
781  ---------+---------+---------+---------+---------+---------+ 840
     TACCTGTACACAgGCAAACTATGCCATCGCGCGTGGTCGCTGCGTTCAGTCGACAGTGGC

     F  C  Q  L  F  T  H  N  E  W  K  K  Y  D  Y  L  Q  S  L  G       300
     TTCTGTCAACTCTTCACTCACAATGAGTGGAAGAAGTACgACTACCTTCAGTCCTTGGGC
841  ---------+---------+---------+---------+---------+---------+ 900
     AAGACAGTTGAGAAGTGAGTGTTACTCACCTTCTTCATGcTGATGGAAGTCAGGAACCCG

     K  Y  Y  G  Y  G  A  G  N  P  L  G  P  A  Q  G  I  G  F  T       320
     AAGTACTACGGCTACGGCGCAGGCAACCCTCTGGGACCGGCTCAGGGGATAGGGTTCACC
901  ---------+---------+---------+---------+---------+---------+ 960
     TTCATGATGCCGATGCCGCGTCCGTTGGGAGACCCTGGCCGAGTCCCCTATCCCAAGTGG

     N  E  L  I  A  R  L  T  R  S  P  V  Q  D  H  T  S  T  N  S       340
     AACGAGCTGATTGCCCGGTTGACgCGTTCGCCAGTGCAGGACCACACCAGCACTAACTCG
961  ---------+---------+---------+---------+---------+---------+ 1020
     TTGCTCGACTAACGGGCCAACTGcGCAAGCGGTCACGTCCTGGTGTGGTCGTGATTGAGC

     T  L  V  S  N  P  A  T  F  P  L  N  A  T  M  Y  V  D  F  S       360
     ACTCTAGTCTCCAACCCGGCCACCTTCCCGTTGAACGCTACCATGTACGTCGACTTTTCA
1021 ---------+---------+---------+---------+---------+---------+ 1080
     TGAGATCAGAGGTTGGGCCGGTGGAAGGGCAACTTGCGATGGTACATGCAGCTGAAAAGT

     H  D  N  S  M  V  S  I  F  F  A  L  G  L  Y  N  G  T  E  P       380
     CACGACAACAGCATGGTTTCCATCTTCTTTGCATTGGGCCTGTACAACGGCACTGAACCC
1081 ---------+---------+---------+---------+---------+---------+ 1140
     GTGCTGTTGTCGTACCAAAGGTAGAAGAAACGTAACCCGGACATGTTGCCGTGACTTGGG

     L  S  R  T  S  V  E  S  A  K  E  L  D  G  Y  S  A  S  W  V       400
     TTGTCCCGGACCTCGGTGGAAAGCGCCAAGGAATTGGATGGGTATTCTGCATCCTGGGTG
1141 ---------+---------+---------+---------+---------+---------+ 1200
     AACAGGGCCTGGAGCCACCTTTCGCGGTTCCTTAACCTACCCATAAGACGTAGGACCCAC

     V  P  F  G  A  R  A  Y  F  E  T  M  Q  C  K  S  E  K  E  P       420
     GTGCCTTTCGGCGCGCGAGCCTACTTCGAGACGATGCAATGCAAGTCGGAAAAGGAGCCT
1201 ---------+---------+---------+---------+---------+---------+ 1260
     CACGGAAAGCCGCGCGCTCGGATGAAGCTCTGCTACGTTACGTTCAGCCTTTTCCTCGGA

     L  V  R  A  L  I  N  D  R  V  V  P  L  H  G  C  D  V  D  K       440
     CTTGTTCGCGCTTTGATTAATGACCGGGTTGTGCCACTGCATGGCTGCGATGTGGACAAG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     GAACAAGCGCGAAACTAATTACTGGCCCAACACGGTGACGTACCGACGCTACACCTGTTC
```

Fig. 9b

```
     L  G  R  C  K  L  N  D  F  V  K  G  L  S  W  A  R  S  G  G   460
     CTGGGGCGATGCAAGCTGAATGACTTTGTCAAGGGATTGAGTTGGGCCAGATCTGGGGGC
1321 ---------+---------+---------+---------+---------+---------+ 1380
     GACCCCGCTACGTTCGACTTACTGAAACAGTTCCCTAACTCAACCCGGTCTAGACCCCCG

     N  W  G  E  C  F  S  *   467
     AACTGGGGAGAGTGCTTTAGTTGA
1381 ---------+---------+---- 1404
     TTGACCCCTCTCACGAAATCAACT
```


Fig. 9c

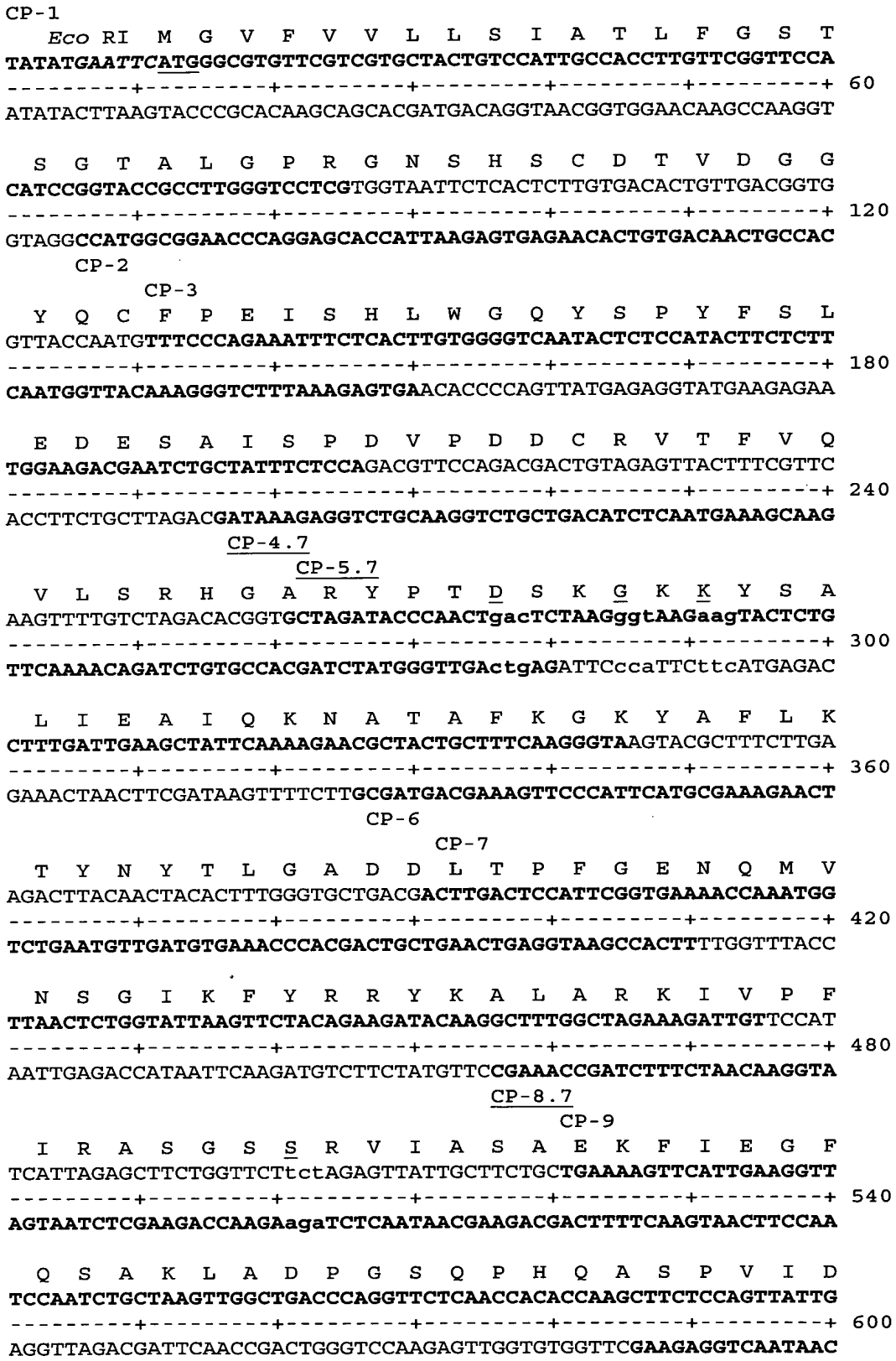


Fig. 10a

```
                                                 CP-10.7
                                                      CP-11.7
       V  I  I  S  E  A  S  S  Y  N  N  T  L  D  P  G  T  C  T  A
      ACGTTATTATTtctGAcgctTCTtctTACAACAACACTTTGGACccaGGTACTTGTACTG
 601  ---------+---------+---------+---------+---------+---------+ 660
      TGCAATAATAAagaCTgcgaAGGagaATGTTGTTGTGAAACCTGggtCCATGAACATGAC

       F  E  D  S  E  L  A  D  T  V  E  A  N  F  T  A  L  F  A  P
      CTTTCGAAGACTCTGAATTGgctGACactGTTGAAGCTAACTTCACTGCTTTGTTCGCTC
 661  ---------+---------+---------+---------+---------+---------+ 720
      GAAAGCTTCTGAGACTTAACcgaCTGtgaCAACTTCGATTGAAGTGACGAAACAAGCGAG
                                                          CP-12.7

       A  I  R  A  R  L  E  A  D  L  P  G  V  T  L  T  D  T  E  V
      CAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACactgaaG
 721  ---------+---------+---------+---------+---------+---------+ 780
      GTCGATAATCTCGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGtgacttC

      CP-13.7
       T  Y  L  M  D  M  C  S  F  E  T  V  A  R  T  S  D  A  T  E
      TTactTACTTGATGGACATGTGTtctTTCGAAACTGTTGCTAGAACTTCTGACGCTACTG
 781  ---------+---------+---------+---------+---------+---------+ 840
      AAtgaATGAACTACCTGTACACAagaAAGCTTTGACAACGATCTTGAAGACTGCGATGAC

       L  S  P  F  C  A  L  F  T  H  D  E  W  R  H  Y  D  Y  L  Q
      AATTGTCTCCATTCTGTGCTTTGTTCACTCACGACGAATGGAGAcacTACGACTACTTGC
 841  ---------+---------+---------+---------+---------+---------+ 900
      TTAACAGAGGTAAGACACGAAACAAGTGAGTGCTGCTTACCTCTgtgATGCTGATGAACG
           CP-14.7
               CP-15.7
       S  L  K  K  Y  Y  G  H  G  A  G  N  P  L  G  P  T  Q  G  V
      AATCTTTGaagAAGTACTACGGTcacGGTGCTGGTAACCCATTGGGTCCAactCAAGGTG
 901  ---------+---------+---------+---------+---------+---------+ 960
      TTAGAAACttcTTCATGATGCCAgtgCCACGACCATTGGGTAACCCAGGTtgaGTTCCAC

       G  F  A  N  E  L  I  A  R  L  T  R  S  P  V  Q  D  H  T  S
      TTGGTTTCGCTAACGAATTGATTGCTAGATTGACTAGATCTCCAGTTCAAGACCACACTT
 961  ---------+---------+---------+---------+---------+---------+ 1020
      AACCAAAGCGATTGCTTAACTAACGATCTAACTGATCTAGAGGTCAAGTTCTGGTGTGAA
                   CP-16
                      CP-17.7
       T  N  H  T  L  D  S  N  P  A  T  F  P  L  N  A  T  L  Y  A
      CTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACG
1021  ---------+---------+---------+---------+---------+---------+ 1080
      GATGATTGGTGTGAAACCTGAGATTGGGTCGATGAAAGGGTAACTTGCGATGAAACATGC

       D  F  S  H  D  N  G  I  I  S  I  F  F  A  L  G  L  Y  N  G
      CTGACTTCTCTCACGACAACggtattATTTCTATTTTCTTCGCTTTGGGTTTGTACAACG
1081  ---------+---------+---------+---------+---------+---------+ 1140
      GACTGAAGAGAGTGCTGTTGccataaTAAAGATAAAAGAAGCGAAACCCAAACATGTTGC
                                  CP-18.7
                                     CP-19.7
       T  A  P  L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  S  S
      GTACTGCTCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTt
1141  ---------+---------+---------+---------+---------+---------+ 1200
      CATGACGAGGTAACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGAa
```

Fig. 10b

```
      A  W  T  V  P  F  A  S  R  A  Y  V  E  M  M  Q  C  Q  A  E
     ctgctTGGACTGTTCCATTCgcttctAGAGCTTACGTTGAAATGATGCAATGTCAAGCTG
1201 ---------+---------+---------+---------+---------+---------+ 1260
     gacgaACCTGACAAGGTAAGcgaagaTCTCGAATGCAACTTTACTACGTTACAGTTCGAC
                                       CP-20
                                            CP-21

      K  E  P  L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  A
     AAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTTCCTTGGTAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC

      V  D  K  L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R
     CTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     GACAACTGTTCAACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGAT
                                                      CP-22

      S  G  G  N  W  A  E  C  F  A  *  Eco RI
     GATCTGGTGGTAACTGGGCTGAATGTTTCGCTTAAGAATTCATATA
1381 ---------+---------+---------+---------+------ 1426
     CTAGACCACCATTGACCCGACTTACAAAGCGAATTCTTAAGTATAT
```


Fig. 10c

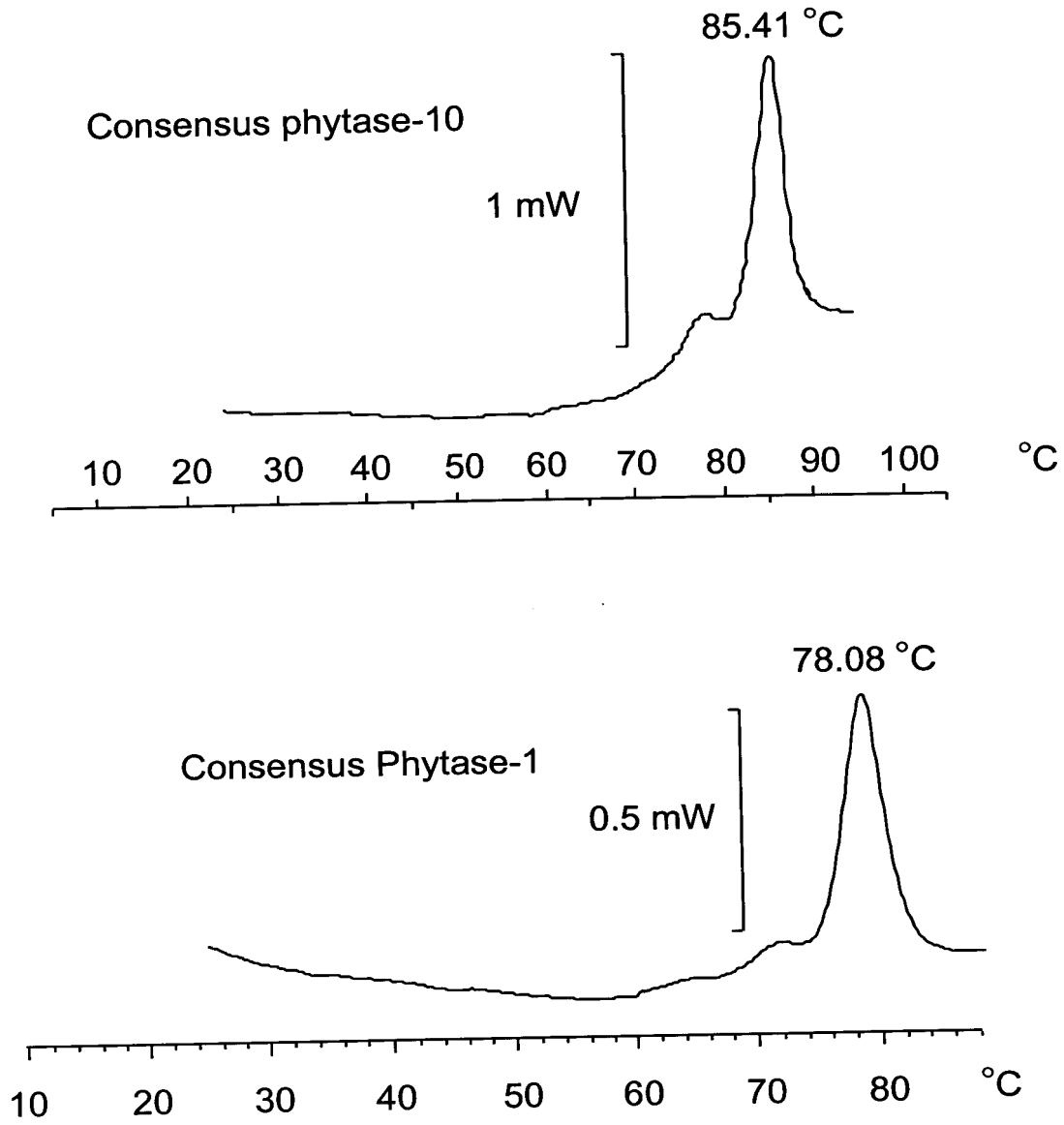


Fig. 11

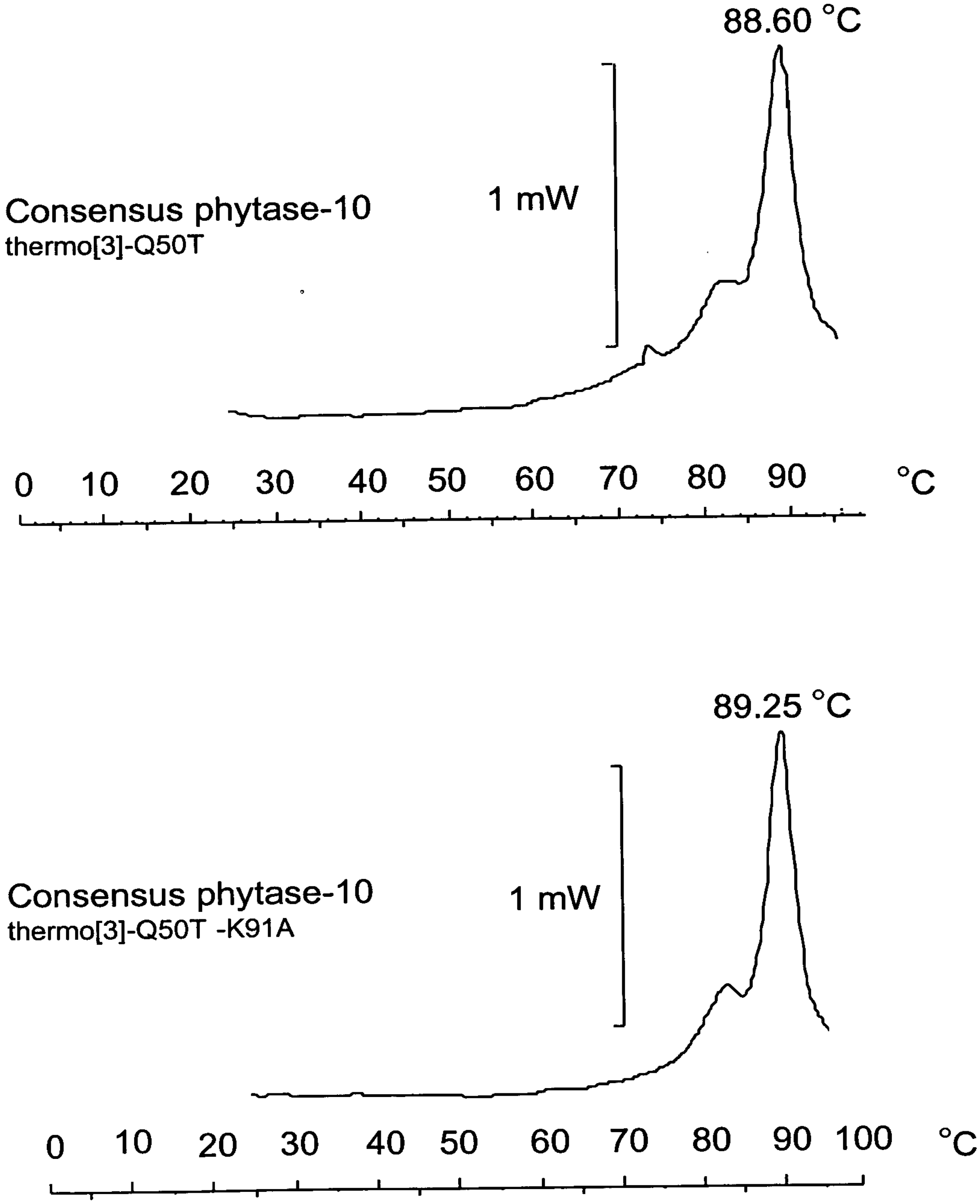


Fig. 12

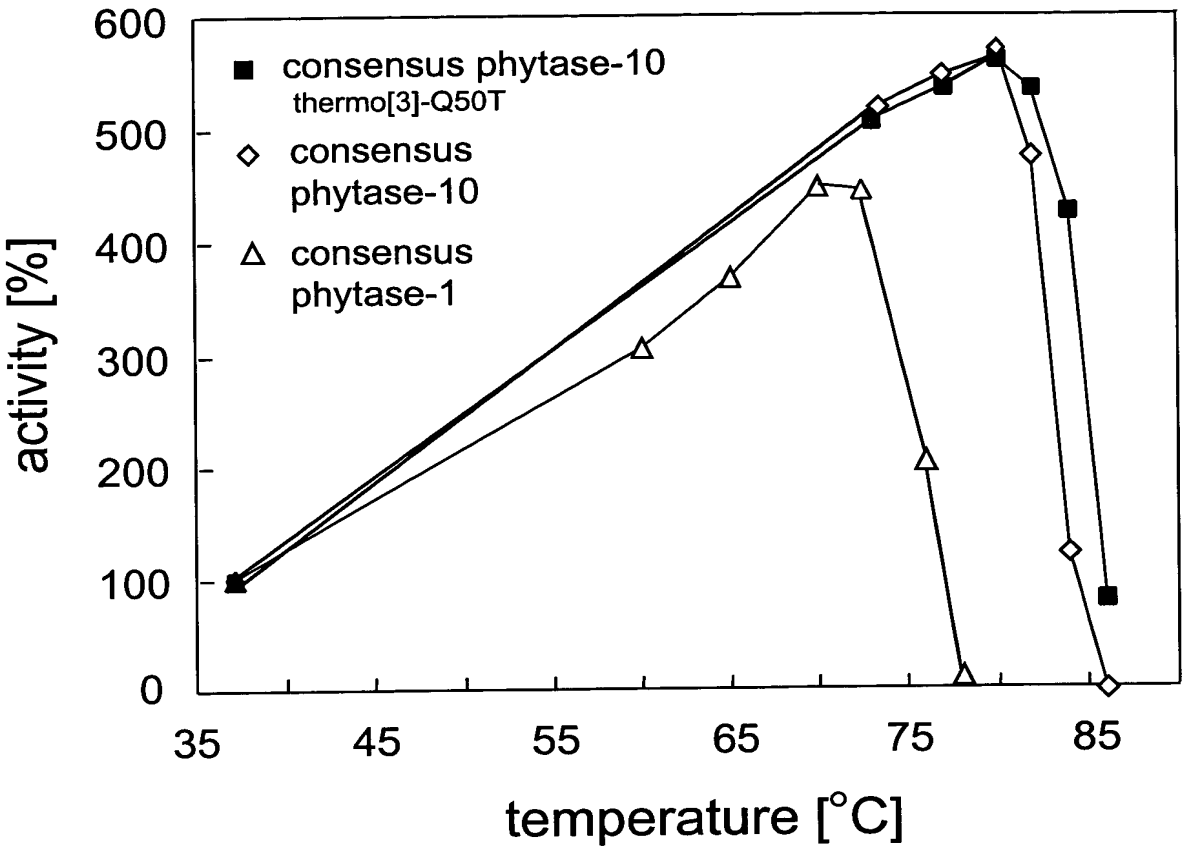


Fig. 13

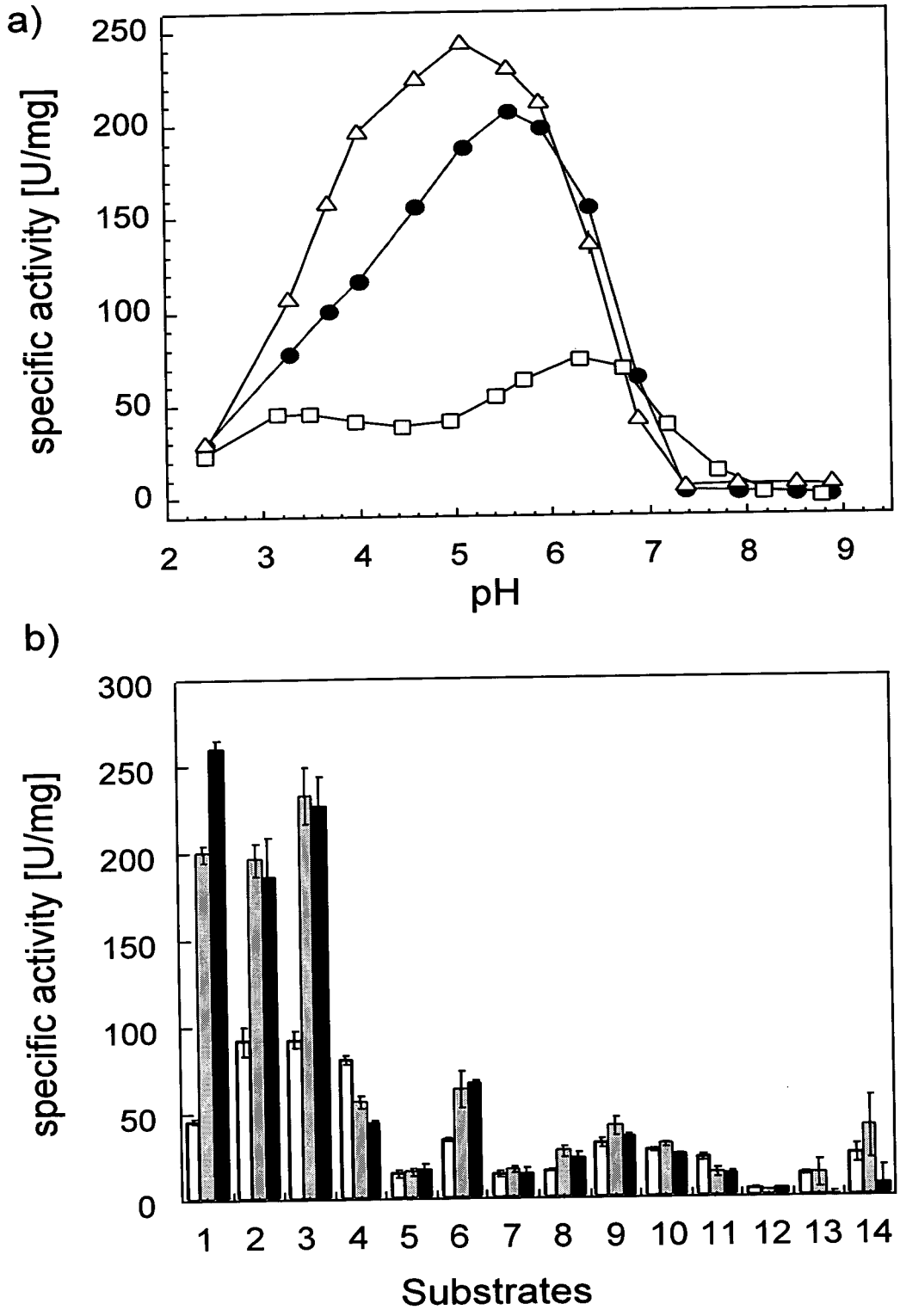
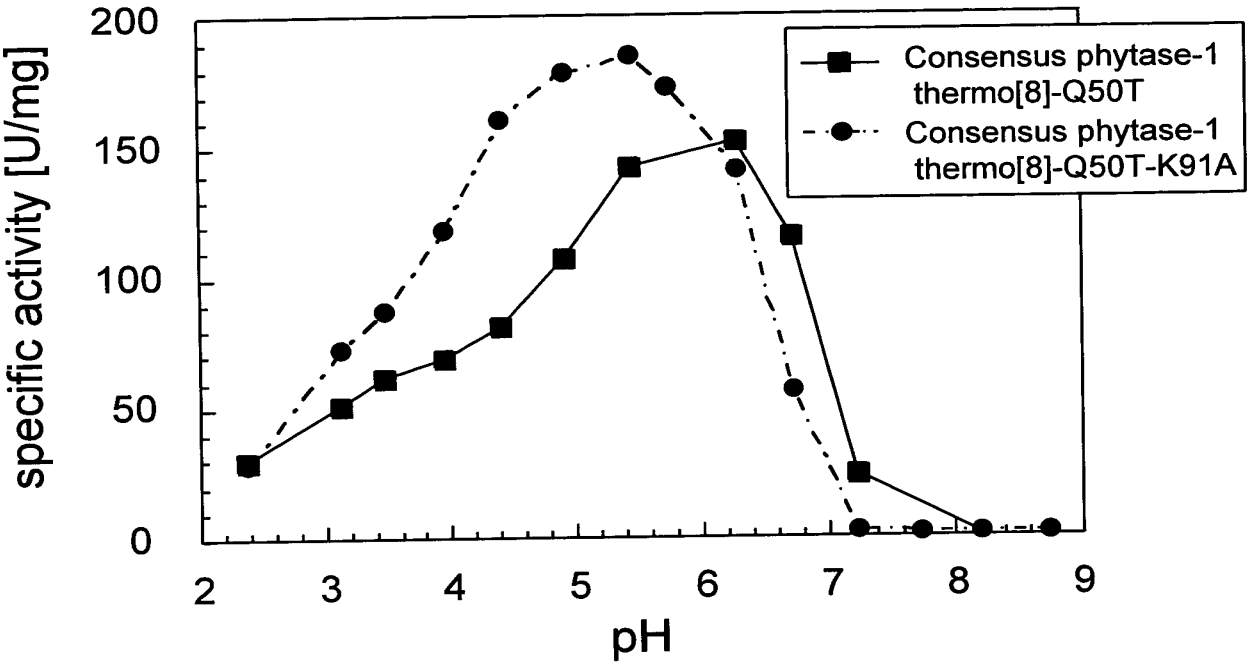


Fig. 14



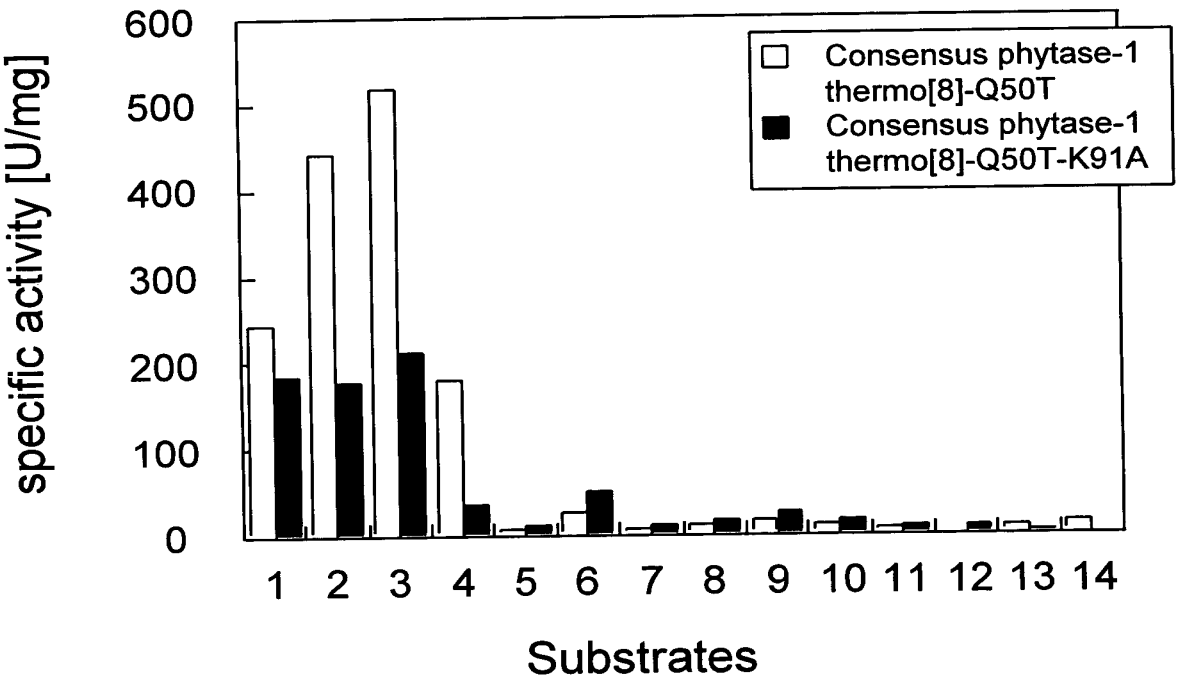


Fig. 15

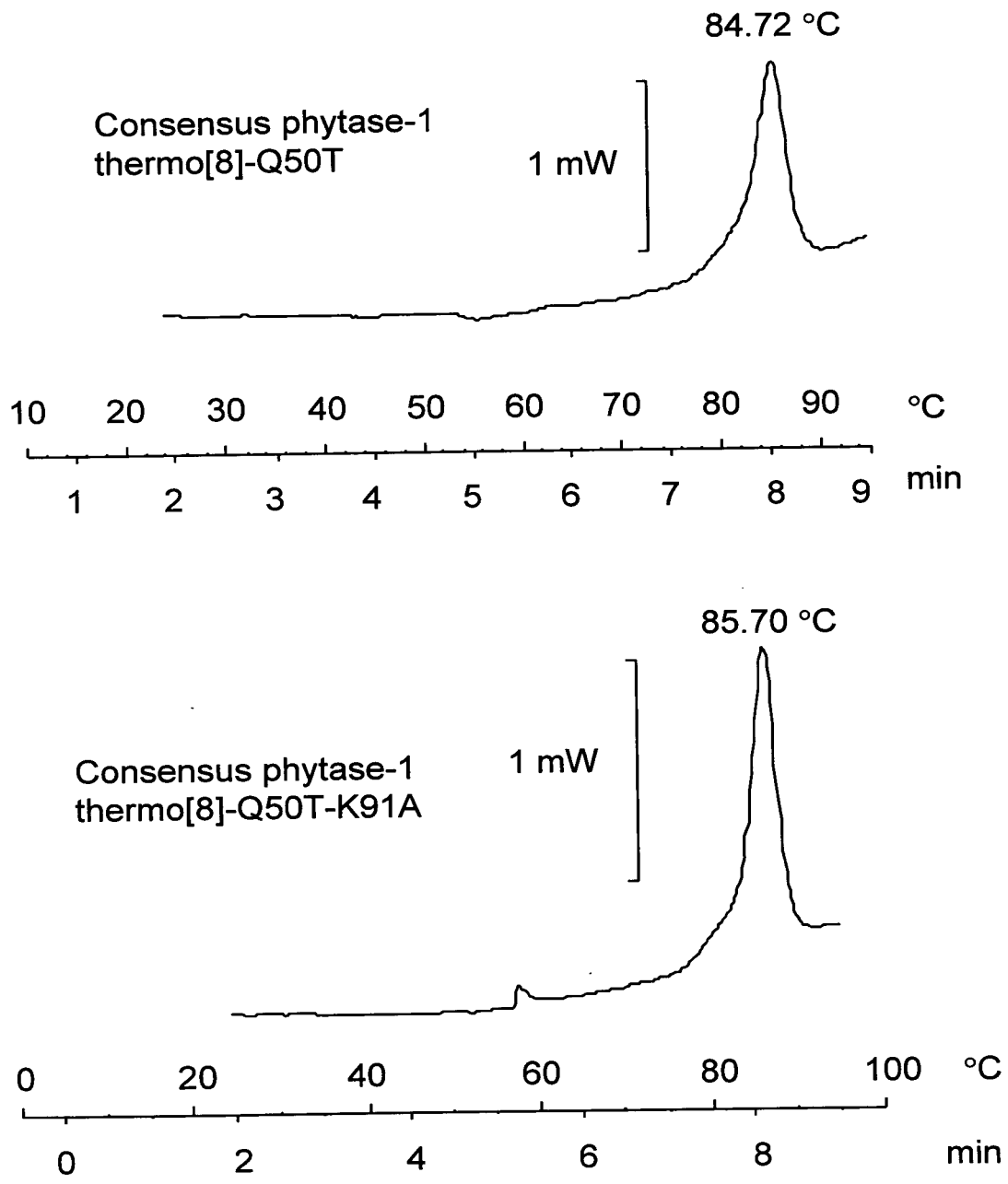


Fig. 16

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

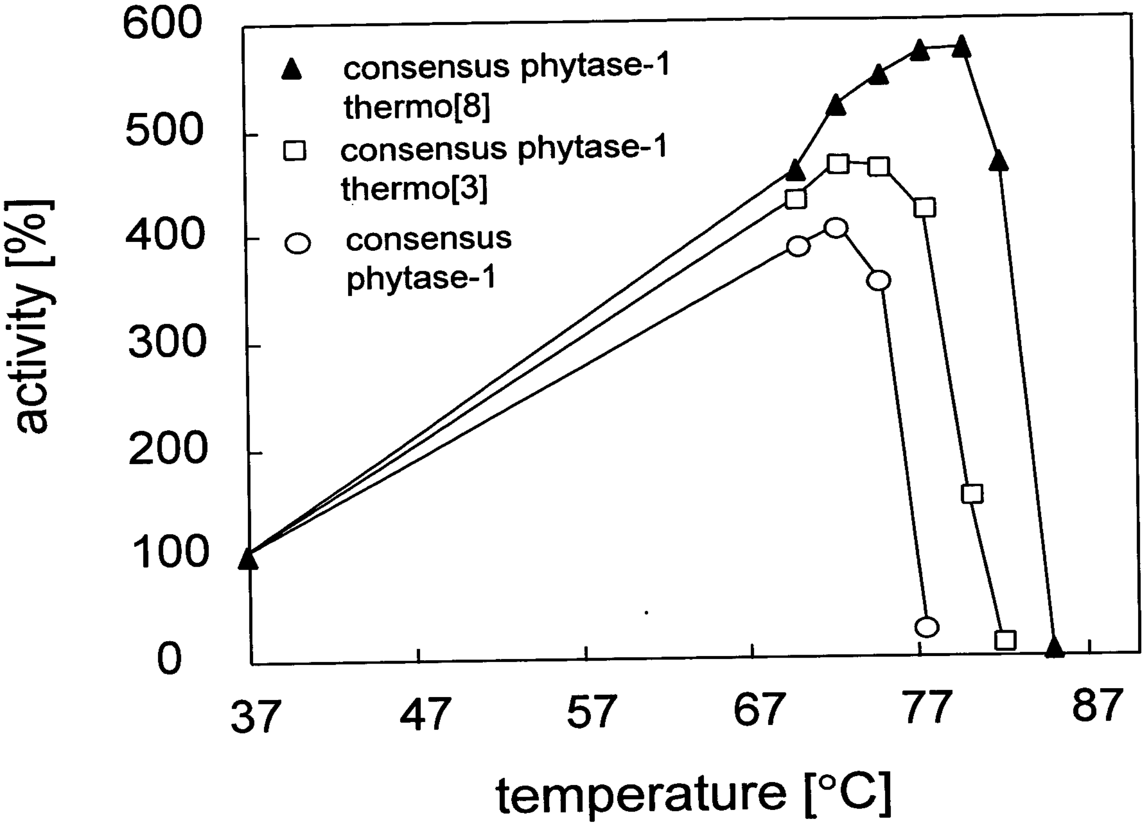
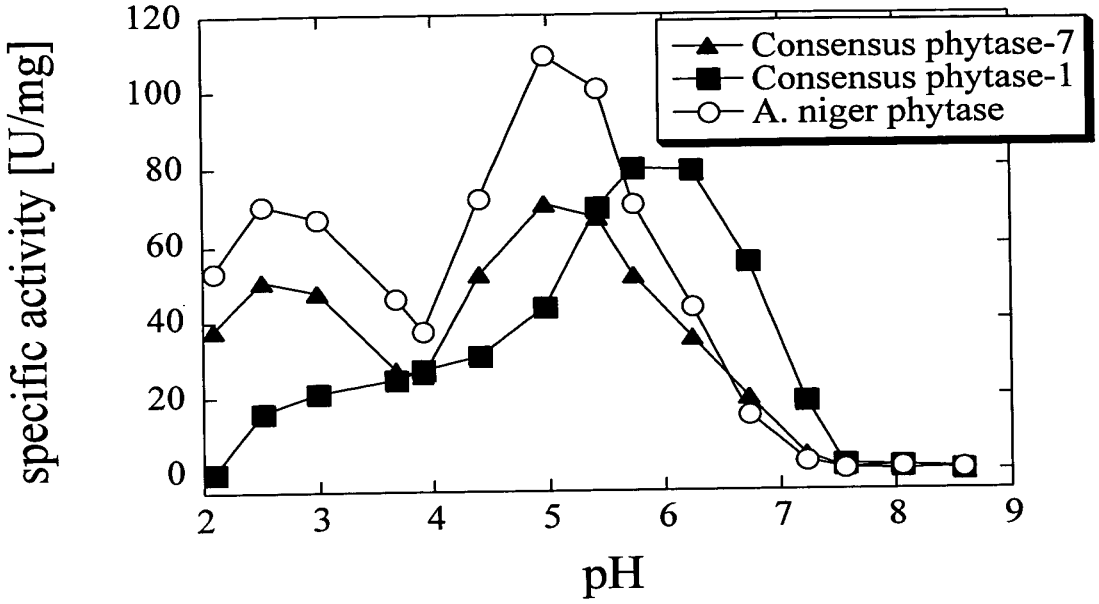


Fig. 17



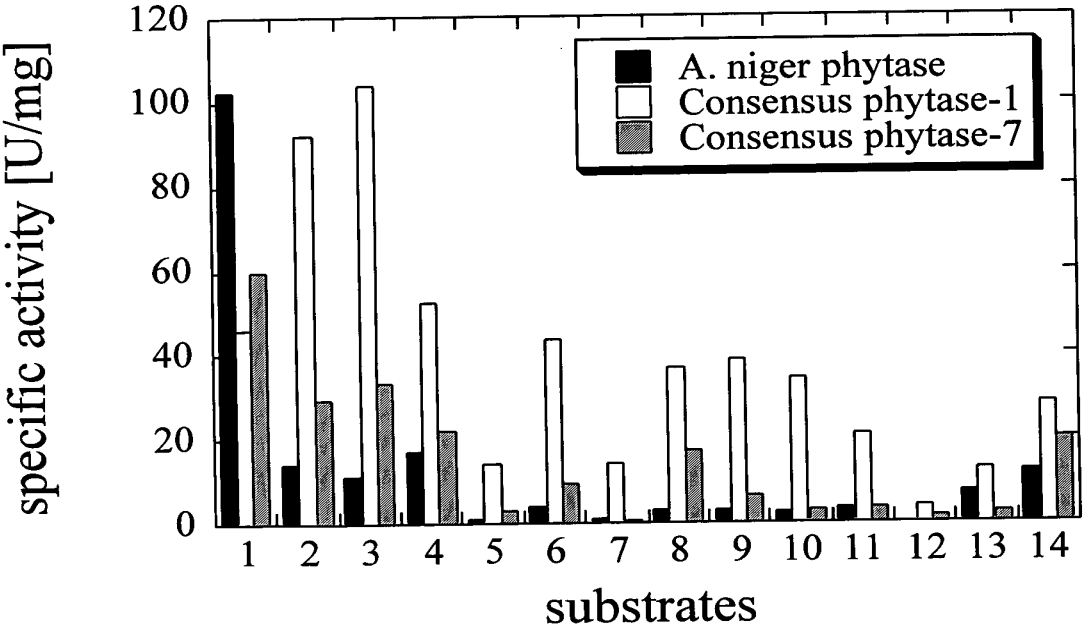


Fig. 18

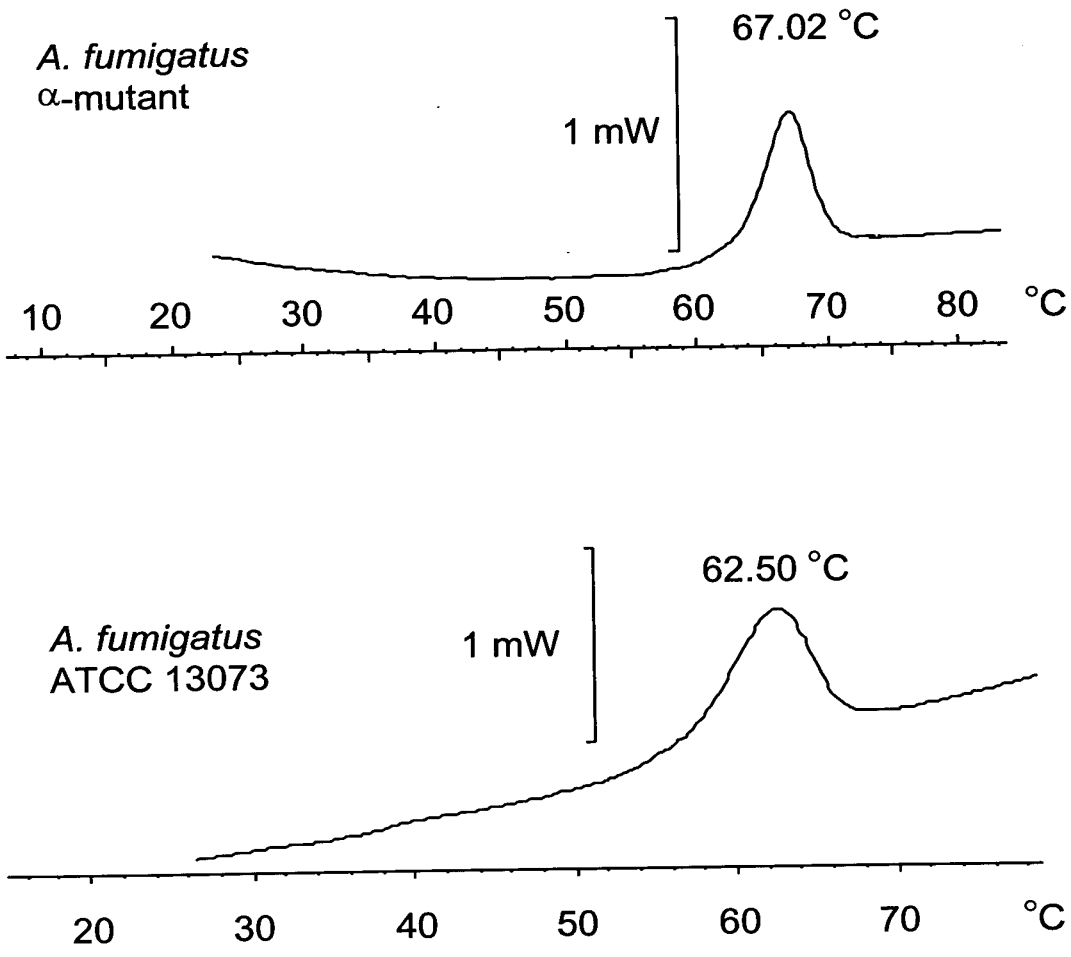


Fig. 19

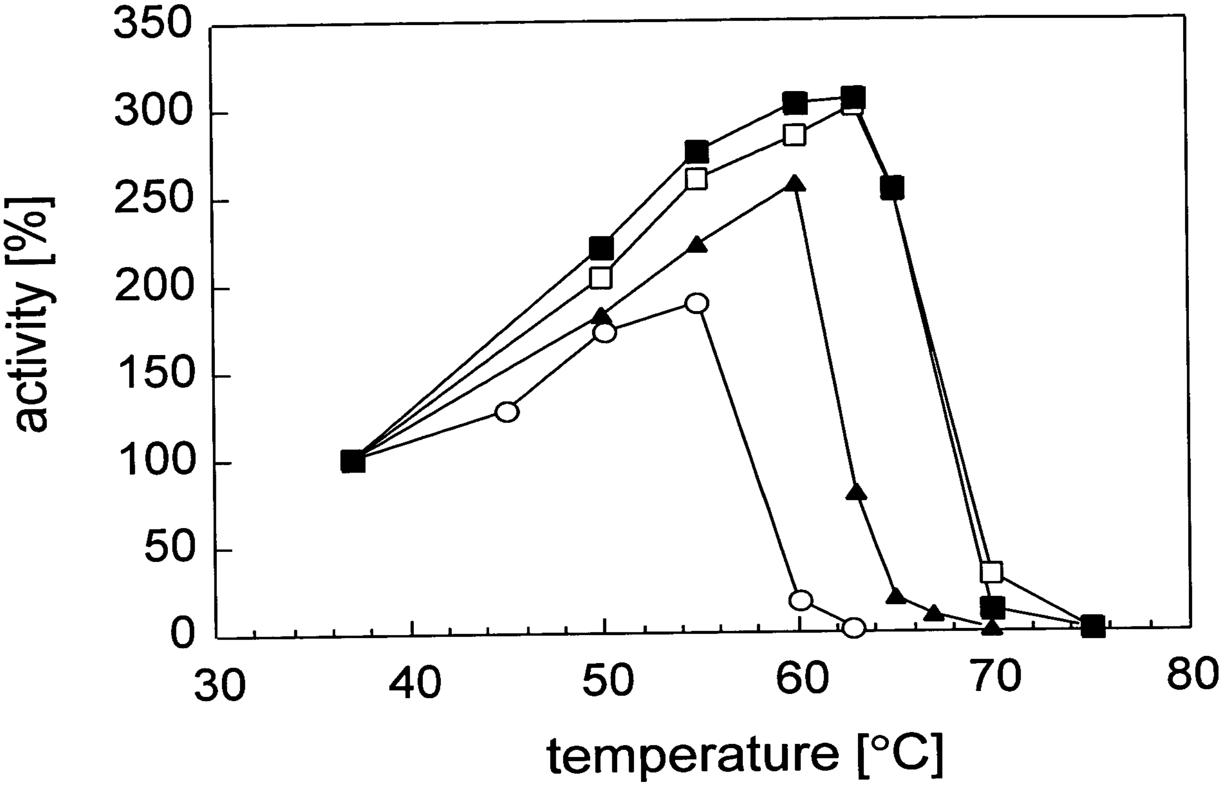


Fig. 20

1 MGVFVVLLSI ATLFGSTSGT ALGPRGNSHS CDTVDGGYQC FPEISSNWSP

51 YSPYFSLADE SAISPDVPKG CRVTFVQVLQ RHGARFPTSG AATRISALIE

101 AIQKNATAFK GKYAFLKTYN YTLGADDLVP FGANQSSQAG IKFYRRYKAL

151 ARKIVPFIRA SGSDRVIDSA TNWIEGFQSA KLADPGANPH QASPVINVII

201 PEGAGYNNTL DHGLCTAFEE SELGDDVEAN FTAVFAPPIR ARLEAHLPGV

251 NLTDEDVVNL MDMCPFDTVA RTSDATELSP FCDLFTHDEW IQYDYLGDLD

301 KYYGTGAGNP LGPAQGVGFV NELIARLTHS PVQDHTSTNH TLDSNPATFP

351 LNATLYADFS HDNTMVAIFF ALGLYNGTKP LSTTSVESIE ETDGYSASWL

401 VPFSARMYVE MMQCEAEKEP LVRVLVNDRV VPLHGCGVDK LGRCKRDDFV

451 EGLSFARSGG NWEECFA

Fig. 21

```
      ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC
   1  ---------+---------+---------+---------+---------+---------+ 60
      TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGTGTAGGCCATGG

      M  G  V  F  V  V  L  L  S  I  A  T  L  F  G  S  T  S  G  T  -

      GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
  61  ---------+---------+---------+---------+---------+---------+ 120
      CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

      A  L  G  P  R  G  N  S  H  S  C  D  T  V  D  G  G  Y  Q  C  -

      TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA
 121  ---------+---------+---------+---------+---------+---------+ 180
      AAGGGTCTTTAAAGAGTGAACACCCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT

      F  P  E  I  S  H  L  W  G  T  Y  S  P  Y  F  S  L  A  D  E  -

      TCTGCTATTTCTCCAGACGTCCCAAAGGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT
 181  ---------+---------+---------+---------+---------+---------+ 240
      AGACGATAAAGAGGTCTGCAGGGTTTCCTGACATCTCAATGAAAGCAAGTTCAAAACAGA

      S  A  I  S  P  D  V  P  K  D  C  R  V  T  F  V  Q  V  L  S  -

      AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGGCTTACTCTGCTTTGATTGAA
 241  ---------+---------+---------+---------+---------+---------+ 300
      TCTGTGCCACGATCTATGGGTTGAAGAAGATTCAGATTCCGAATGAGACGAAACTAACTT

      R  H  G  A  R  Y  P  T  S  S  K  S  K  A  Y  S  A  L  I  E  -

      GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
 301  ---------+---------+---------+---------+---------+---------+ 360
      CGATAAGTTTTCTTGCGATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTG

      A  I  Q  K  N  A  T  A  F  K  G  K  Y  A  F  L  K  T  Y  N  -

      TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT
 361  ---------+---------+---------+---------+---------+---------+ 420
      ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTTGGTTTACCAATTGAGACCA

      Y  T  L  G  A  D  D  L  T  P  F  G  E  N  Q  M  V  N  S  G  -

      ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT
 421  ---------+---------+---------+---------+---------+---------+ 480
      TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

      I  K  F  Y  R  R  Y  K  A  L  A  R  K  I  V  P  F  I  R  A  -

      TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT
 481  ---------+---------+---------+---------+---------+---------+ 540
      AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAAAGGTTAGACGA

      S  G  S  D  R  V  I  A  S  A  E  K  F  I  E  G  F  Q  S  A  -
```

Fig. 22a

```
     AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT
541  ---------+---------+---------+---------+---------+---------+ 600
     TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTCGAAGAGGTCAATAATTGCACTAGTAA

     K  L  A  D  P  G  S  Q  P  H  Q  A  S  P  V  I  N  V  I  I  -

     CCAGAAGGATCCGGTTACAACAACACTTTGGACCATGGTCTTTGTACTGCTTTCGAAGAC
601  ---------+---------+---------+---------+---------+---------+ 660
     GGTCTTCCTAGGCCAATGTTGTTGTGAAACCTGGTACCAGAAACATGACGAAAGCTTCTG

     P  E  G  S  G  Y  N  N  T  L  D  H  G  L  C  T  A  F  E  D  -

     TCTACCCTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA
661  ---------+---------+---------+---------+---------+---------+ 720
     AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAGGTCGATAATCT

     S  T  L  G  D  D  V  E  A  N  F  T  A  L  F  A  P  A  I  R  -

     GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG
721  ---------+---------+---------+---------+---------+---------+ 780
     CGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGCTTCTGCAACAAATGAAC

     A  R  L  E  A  D  L  P  G  V  T  L  T  D  E  D  V  V  Y  L  -

     ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA
781  ---------+---------+---------+---------+---------+---------+ 840
     TACCTGTACACAGGTAAGCTGTGACAGCGATCTTGAAGACTGCGATGACTTAACAGAGGT

     M  D  M  C  P  F  D  T  V  A  R  T  S  D  A  T  E  L  S  P  -

     TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT
841  ---------+---------+---------+---------+---------+---------+ 900
     AAGACACGAAACAAGTGAGTGCTGCTTACCTAGGTTATGCTGATGAACGTTTCGAACCCA

     F  C  A  L  F  T  H  D  E  W  I  Q  Y  D  Y  L  Q  S  L  G  -

     AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT
901  ---------+---------+---------+---------+---------+---------+ 960
     TTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTCGAGTTCCACAACCAAAGCGA

     K  Y  Y  G  Y  G  A  G  N  P  L  G  P  A  Q  G  V  G  F  A  -

     AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961  ---------+---------+---------+---------+---------+---------+ 1020
     TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

     N  E  L  I  A  R  L  T  H  S  P  V  Q  D  H  T  S  T  N  H  -

     ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
1021 ---------+---------+---------+---------+---------+---------+ 1080
     TGAAACCTGAGATTGGGTCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

     T  L  D  S  N  P  A  T  F  P  L  N  A  T  L  Y  A  D  F  S  -
```


Fig. 22b

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS


```
     CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA
1081 ---------+---------+---------+---------+---------+---------+ 1140
     GTGCTGTTGTGATACTATAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGGTTCGGT

     H  D  N  T  M  I  S  I  F  F  A  L  G  L  Y  N  G  T  K  P  -

     TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT
1141 ---------+---------+---------+---------+---------+---------+ 1200
     AACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

     L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  S  A  S  W  T  -

     GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA
1201 ---------+---------+---------+---------+---------+---------+ 1260
     CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACAGTTCGACTTTTCCTTGGT

     V  P  F  A  A  R  A  Y  V  E  M  M  Q  C  Q  A  E  K  E  P  -

     TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACTGTTC

     L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  A  V  D  K  -

     TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321 ---------+---------+---------+---------+---------+---------+ 1380
     AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

     L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G  -

     AACTGGGCTGAATGTTTCGCTTAA
1381 ---------+---------+---- 1404
     TTGACCCGACTTACAAAGCGAATT

     N  W  A  E  C  F  A  *
```


Fig. 22c

```
     ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC
  1  ---------+---------+---------+---------+---------+---------+ 60
     TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGTGTAGGCCATGG

     M  G  V  F  V  V  L  L  S  I  A  T  L  F  G  S  T  S  G  T  -

     GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
 61  ---------+---------+---------+---------+---------+---------+ 120
     CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

     A  L  G  P  R  G  N  S  H  S  C  D  T  V  D  G  G  Y  Q  C  -

     TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA
121  ---------+---------+---------+---------+---------+---------+ 180
     AAGGGTCTTTAAAGAGTGAACACCCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT

     F  P  E  I  S  H  L  W  G  T  Y  S  P  Y  F  S  L  A  D  E  -

     TCTGCTATTTCTCCAGACGTCCCAAAGGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT
181  ---------+---------+---------+---------+---------+---------+ 240
     AGACGATAAAGAGGTCTGCAGGGTTTCCTGACATCTCAATGAAAGCAAGTTCAAAACAGA

     S  A  I  S  P  D  V  P  K  D  C  R  V  T  F  V  Q  V  L  S  -

     AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA
241  ---------+---------+---------+---------+---------+---------+ 300
     TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGAATGAGACGAAACTAACTT

     R  H  G  A  R  Y  P  T  S  S  A  S  K  A  Y  S  A  L  I  E  -

     GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
301  ---------+---------+---------+---------+---------+---------+ 360
     CGATAAGTTTTCTTGCGATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTG

     A  I  Q  K  N  A  T  A  F  K  G  K  Y  A  F  L  K  T  Y  N  -

     TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT
361  ---------+---------+---------+---------+---------+---------+ 420
     ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTTGGTTTACCAATTGAGACCA

     Y  T  L  G  A  D  D  L  T  P  F  G  E  N  Q  M  V  N  S  G  -

     ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT
421  ---------+---------+---------+---------+---------+---------+ 480
     TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

     I  K  F  Y  R  R  Y  K  A  L  A  R  K  I  V  P  F  I  R  A  -

     TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481  ---------+---------+---------+---------+---------+---------+ 540
     AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAAAGGTTAGACGA

     S  G  S  D  R  V  I  A  S  A  E  K  F  I  E  G  F  Q  S  A  -
```

Fig. 23a

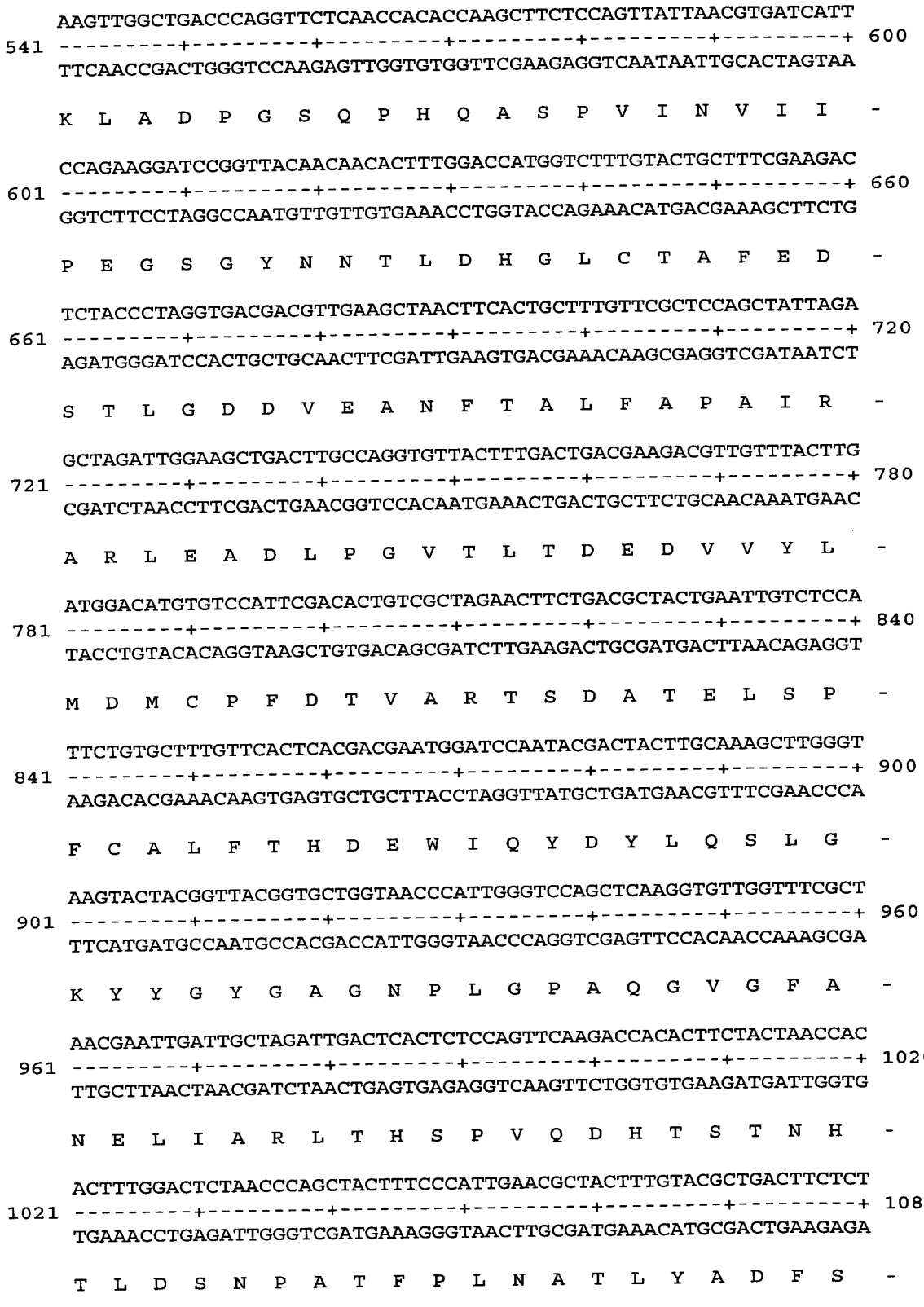


Fig. 23b

```
     CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA
1081 ---------+---------+---------+---------+---------+---------+ 1140
     GTGCTGTTGTGATACTATAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGGTTCGGT

     H  D  N  T  M  I  S  I  F  F  A  L  G  L  Y  N  G  T  K  P  -

     TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT
1141 ---------+---------+---------+---------+---------+---------+ 1200
     AACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

     L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  S  A  S  W  T  -

     GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA
1201 ---------+---------+---------+---------+---------+---------+ 1260
     CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACAGTTCGACTTTTCCTTGGT

     V  P  F  A  A  R  A  Y  V  E  M  M  Q  C  Q  A  E  K  E  P  -

     TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACTGTTC

     L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  A  V  D  K  -

     TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321 ---------+---------+---------+---------+---------+---------+ 1380
     AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

     L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G  -

     AACTGGGCTGAATGTTTCGCTTAA
1381 ---------+---------+---- 1404
     TTGACCCGACTTACAAAGCGAATT

     N  W  A  E  C  F  A  *
```

Fig. 23c

```
    ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC
  1 ---------+---------+---------+---------+---------+---------+ 60
    TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGTGTAGGCCATGG

    M  G  V  F  V  V  L  L  S  I  A  T  L  F  G  S  T  S  G  T  -

    GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
 61 ---------+---------+---------+---------+---------+---------+ 120
    CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

    A  L  G  P  R  G  N  S  H  S  C  D  T  V  D  G  G  Y  Q  C  -

    TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA
121 ---------+---------+---------+---------+---------+---------+ 180
    AAGGGTCTTTAAAGAGTGAACACCCCATGTATGAGAGGTAAGAAGAGAAACCGACTGCTT

    F  P  E  I  S  H  L  W  G  T  Y  S  P  F  F  S  L  A  D  E  -

    TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT
181 ---------+---------+---------+---------+---------+---------+ 240
    AGACGATAAAGAGGTCTGCAAGGTTTCCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

    S  A  I  S  P  D  V  P  K  G  C  R  V  T  F  V  Q  V  L  S  -

    AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGGCTTACTCTGCTTTGATTGAA
241 ---------+---------+---------+---------+---------+---------+ 300
    TCTGTGCCACGATCTATGGGTTGAAGAAGATTCAGATTCCGAATGAGACGAAACTAACTT

    R  H  G  A  R  Y  P  T  S  S  K  S  K  A  Y  S  A  L  I  E  -

    GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAT
301 ---------+---------+---------+---------+---------+---------+ 360
    CGATAAGTTTTCTTGCGATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTA

    A  I  Q  K  N  A  T  A  F  K  G  K  Y  A  F  L  K  T  Y  N  -

    TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT
361 ---------+---------+---------+---------+---------+---------+ 420
    ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTGTTGTTTACCAATTGAGACCA

    Y  T  L  G  A  D  D  L  T  P  F  G  E  Q  Q  M  V  N  S  G  -

    ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT
421 ---------+---------+---------+---------+---------+---------+ 480
    TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

    I  K  F  Y  R  R  Y  K  A  L  A  R  K  I  V  P  F  I  R  A  -

    TCTGGTTCTGACAGAGTTATTGCTTCTGCCGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481 ---------+---------+---------+---------+---------+---------+ 540
    AGACCAAGACTGTCTCAATAACGAAGACGGCTTTTCAAGTAACTTCCAAAGGTTAGACGA

    S  G  S  D  R  V  I  A  S  A  E  K  F  I  E  G  F  Q  S  A  -
```

Fig. 24a

```
     AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT
541  ---------+---------+---------+---------+---------+---------+ 600
     TTCAACCGACTGGGTCCACGATTGGGTGTGGTTCGAAGAGGTCAATAATTGCAATAATAA

     K  L  A  D  P  G  A  N  P  H  Q  A  S  P  V  I  N  V  I  I  -

     CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA
601  ---------+---------+---------+---------+---------+---------+ 660
     GGTCTTCCACGACCAATGTTGTTGTGAAACCTGGTGCCAAACACATGACGAAAGCTTCTT

     P  E  G  A  G  Y  N  N  T  L  D  H  G  L  C  T  A  F  E  E  -

     TCTACCCTAGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA
661  ---------+---------+---------+---------+---------+---------+ 720
     AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAGGTGGTTAATCT

     S  T  L  G  D  D  V  E  A  N  F  T  A  V  F  A  P  P  I  R  -

     GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG
721  ---------+---------+---------+---------+---------+---------+ 780
     CGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGCAACAATTGAAC

     A  R  L  E  A  H  L  P  G  V  N  L  T  D  E  D  V  V  N  L  -

     ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA
781  ---------+---------+---------+---------+---------+---------+ 840
     TACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAGTTAACAGAGGT

     M  D  M  C  P  F  D  T  V  A  R  T  S  D  A  T  Q  L  S  P  -

     TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT
841  ---------+---------+---------+---------+---------+---------+ 900
     AAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACGTTAGAAACCCA

     F  C  D  L  F  T  H  D  E  W  I  Q  Y  D  Y  L  Q  S  L  G  -

     AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT
901  ---------+---------+---------+---------+---------+---------+ 960
     TTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTCGAGTTCCACAACCAAAGCAA

     K  Y  Y  G  Y  G  A  G  N  P  L  G  P  A  Q  G  V  G  F  V  -

     AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961  ---------+---------+---------+---------+---------+---------+ 1020
     TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

     N  E  L  I  A  R  L  T  H  S  P  V  Q  D  H  T  S  T  N  H  -

     ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
1021 ---------+---------+---------+---------+---------+---------+ 1080
     TGAAACCTGAGATTGGGTCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

     T  L  D  S  N  P  A  T  F  P  L  N  A  T  L  Y  A  D  F  S  -
```


Fig. 24b

```
     CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA
1081 ---------+---------+---------+---------+---------+---------+ 1140
     GTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGATTCGGT

     H  D  N  T  M  V  S  I  F  F  A  L  G  L  Y  N  G  T  K  P   -

     TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT
1141 ---------+---------+---------+---------+---------+---------+ 1200
     AACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

     L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  S  A  S  W  T   -

     GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
1201 ---------+---------+---------+---------+---------+---------+ 1260
     CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACACTTCGACTTTTCCTTGGT

     V  P  F  A  A  R  A  Y  V  E  M  M  Q  C  E  A  E  K  E  P   -

     TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACTGTTC

     L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  A  V  D  K   -

     TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321 ---------+---------+---------+---------+---------+---------+ 1380
     AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

     L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G   -

     AACTGGGAAGAATGTTTCGCTTAA
1381 ---------+---------+---- 1404
     TTGACCCTTCTTACAAAGCGAATT

     N  W  E  E  C  F  A  *
```


Fig. 24c

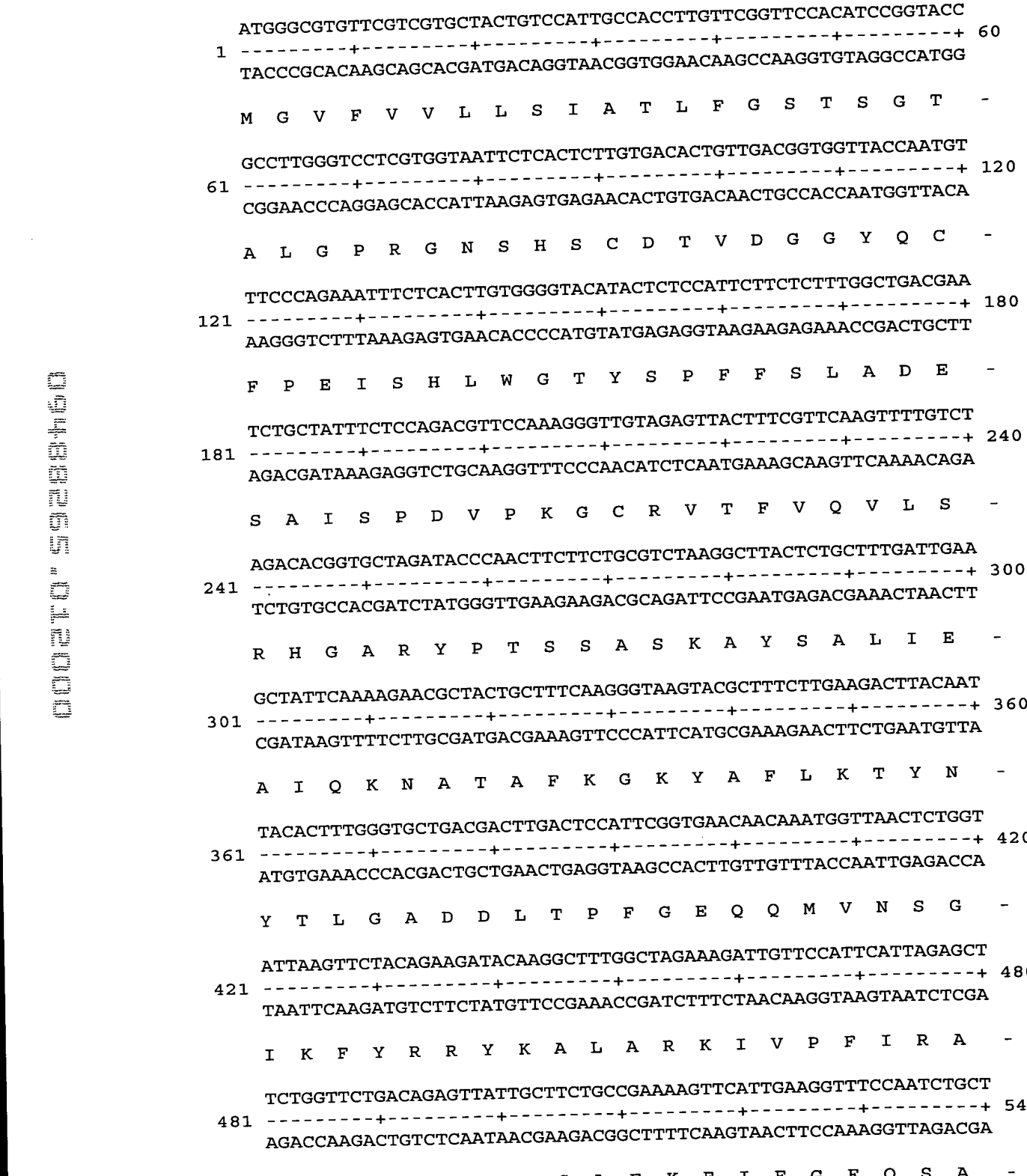


Fig. 25a

AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT
541 ---------+---------+---------+---------+---------+---------+ 600
TTCAACCGACTGGGTCCACGATTGGGTGTGGTTCGAAGAGGTCAATAATTGCAATAATAA

K L A D P G A N P H Q A S P V I N V I I -

CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA
601 ---------+---------+---------+---------+---------+---------+ 660
GGTCTTCCACGACCAATGTTGTTGTGAAACCTGGTGCCAAACACATGACGAAAGCTTCTT

P E G A G Y N N T L D H G L C T A F E E -

TCTACCCTAGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA
661 ---------+---------+---------+---------+---------+---------+ 720
AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAGGTGGTTAATCT

S T L G D D V E A N F T A V F A P P I R -

GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG
721 ---------+---------+---------+---------+---------+---------+ 780
CGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGCAACAATTGAAC

A R L E A H L P G V N L T D E D V V N L -

ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA
781 ---------+---------+---------+---------+---------+---------+ 840
TACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAGTTAACAGAGGT

M D M C P F D T V A R T S D A T Q L S P -

TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT
841 ---------+---------+---------+---------+---------+---------+ 900
AAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACGTTAGAAACCCA

F C D L F T H D E W I Q Y D Y L Q S L G -

AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT
901 ---------+---------+---------+---------+---------+---------+ 960
TTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTCGAGTTCCACAACCAAAGCAA

K Y Y G Y G A G N P L G P A Q G V G F V -

AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961 ---------+---------+---------+---------+---------+---------+ 1020
TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

N E L I A R L T H S P V Q D H T S T N H -

ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
1021 ---------+---------+---------+---------+---------+---------+ 1080
TGAAACCTGAGATTGGGTCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

T L D S N P A T F P L N A T L Y A D F S -

Fig. 25b

```
     CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA
1081 ---------+---------+---------+---------+---------+---------+ 1140
     GTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGATTCGGT

     H  D  N  T  M  V  S  I  F  F  A  L  G  L  Y  N  G  T  K  P   -

     TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT
1141 ---------+---------+---------+---------+---------+---------+ 1200
     AACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

     L  S  T  T  S  V  E  S  I  E  E  T  D  G  Y  S  A  S  W  T   -

     GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
1201 ---------+---------+---------+---------+---------+---------+ 1260
     CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACACTTCGACTTTTCCTTGGT

     V  P  F  A  A  R  A  Y  V  E  M  M  Q  C  E  A  E  K  E  P   -

     TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 ---------+---------+---------+---------+---------+---------+ 1320
     AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACTGTTC

     L  V  R  V  L  V  N  D  R  V  V  P  L  H  G  C  A  V  D  K   -

     TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321 ---------+---------+---------+---------+---------+---------+ 1380
     AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

     L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G   -

     AACTGGGAAGAATGTTTCGCTTAA
1381 ---------+---------+---- 1404
     TTGACCCTTCTTACAAAGCGAATT

     N  W  E  E  C  F  A  *
```


Fig. 25c